

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:02:32 ; Search time 4148.82 Seconds
(without alignments)
10259.034 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcgggaagtga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rnd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	801	81.6	1102	8	MDO251116	AJ251116 Malus dom
2	337	34.3	473	8	AB081094	AB081094 Malus x d
3	116	11.8	1043	8	AB081093	AB081093 Malus x d
4	34	3.5	1014	8	AB055966	AB055966 Rosa rugo
5	30	3.1	17606	9	BX537160	BX537160 Human DNA
6	30	3.1	183353	10	AL935278	AL935278 Mouse DNA
7	29	3.0	1698	8	NTA313873	AJ719873 Nicotiana
8	28	2.9	1256	8	ATPRPHA	M96732 Arabidopsis
9	28	2.9	1410	8	ATPRX1GE	X98113 A.thaliana
10	28	2.9	68291	8	BX897675	BX897675 Neurospor
11	28	2.9	143793	2	AC099530	AC099530 Felis cat
12	28	2.9	153829	2	AC141671	AC141671 Apis mell
13	28	2.9	174010	2	AC129127	AC129127 Rattus no
14	28	2.9	217691	2	AC103052	AC103052 Rattus no
15	28	2.9	262093	2	AC095577	AC095577 Rattus no
16	28	2.9	292004	2	AC127118	AC127118 Rattus no
17	28	2.9	302156	2	AC116977	AC116977 Dictyoste
18	27	2.7	121	6	AX324459	AX324459 Sequence
19	27	2.7	121	6	AX324460	AX324460 Sequence
20	27	2.7	121	6	AX324463	AX324463 Sequence
21	27	2.7	121	6	AX324464	AX324464 Sequence
22	27	2.7	610	8	AB047923	AB047923 Oryza sat
23	27	2.7	698	8	AB089156	AB089156 Houttuyni
24	27	2.7	753	8	ATH245906	AJ245906 Arabidops
25	27	2.7	912	8	AF088912	AF088912 Petunia x
26	27	2.7	959	8	AB007506	AB007506 Triticum
27	27	2.7	980	6	AX146915	AX146915 Sequence
28	27	2.7	1167	6	AR032064	AR032064 Sequence
29	27	2.7	1167	6	AR060347	AR060347 Sequence
30	27	2.7	1167	6	AR351552	AR351552 Sequence
31	27	2.7	1204	9	BC034821	BC034821 Homo sapi
32	27	2.7	1313	9	BC007035	BC007035 Homo sapi
33	27	2.7	1341	9	BC005317	BC005317 Homo sapi
34	27	2.7	1482	5	BC045299	BC045299 Danio rer
35	27	2.7	1547	8	VVLSTSYM	X76892 V.vinifera
36	27	2.7	1648	9	AB055302	AB055302 Macaca fa
37	27	2.7	2031	10	MMU97675	U97675 Mus musculu
38	27	2.7	2131	9	BC009356	BC009356 Homo sapi
39	27	2.7	2580	10	BC046536	BC046536 Mus muscu
40	27	2.7	3629	3	BT010089	BT010089 Drosophil
41	27	2.7	3907	10	BC052708	BC052708 Mus muscu
42	27	2.7	20622	2	AC115609	AC115609 Dictyoste
43	27	2.7	57203	3	AC116989	AC116989 Dictyoste
44	27	2.7	110000	2	PFNAL13_07	Continuation (8 of
45	27	2.7	110000	2	PFNAL6PI_02	Continuation (3 of
46	27	2.7	110000	3	AC116984_2	Continuation (3 of
47	27	2.7	112752	9	AF030876	AF030876 Homo sapi
48	27	2.7	115499	2	AC130963	AC130963 Medicago
49	27	2.7	133095	2	AC146721	AC146721 Medicago
50	27	2.7	137414	2	AC144721	AC144721 Medicago
51	27	2.7	140544	2	AC011798	AC011798 Homo sapi
52	27	2.7	144571	2	BX842683	BX842683 Danio rer
53	27	2.7	149815	10	AC125089	AC125089 Mus muscu
54	27	2.7	170691	9	AC104643	AC104643 Homo sapi
55	27	2.7	173183	2	AC102742	AC102742 Mus muscu
56	27	2.7	174424	6	AX335950	AX335950 Sequence
57	27	2.7	176317	2	AL670857	AL670857 Mus muscu
58	27	2.7	181343	9	U52112	U52112 Homo sapien
59	27	2.7	181573	2	AC020559	AC020559 Mus muscu
60	27	2.7	183648	3	AC117076	AC117076 Dictyoste
61	27	2.7	184520	9	AC009220	AC009220 Homo sapi
62	27	2.7	190168	10	AC127036	AC127036 Mus muscu
63	27	2.7	190790	2	AC122042	AC122042 Mus muscu
64	27	2.7	192420	2	BX511119	BX511119 Danio rer
65	27	2.7	193643	9	AC018644	AC018644 Homo sapi

Pred. No. is the number of results predicted by chance to have a

212	25	2.5	1791	9	BC016867	BC016867 Homo sapi	285	25	2.5	110000	3	AC116984_0	AC116984 Dictyoste
213	25	2.5	1793	9	BC009048	BC009048 Homo sapi	286	25	2.5	110000	3	AC116984_3	Continuation (4 of
214	25	2.5	1836	3	AF332201	AF332201 Caenorhab	287	25	2.5	112733	8	AC146308	Medicago
215	25	2.5	1837	17	AF116609	AF116609 Homo sapi	288	25	2.5	117391	8	AC124964	Medicago
216	25	2.5	1907	5	BC044563	BC044563 Danio rer	289	25	2.5	119927	8	AC146705	Medicago
217	25	2.5	1916	6	AX753502	AX753502 Sequence	290	25	2.5	121143	8	AC144484	Medicago
218	25	2.5	1928	9	BC021121	BC021121 Homo sapi	291	25	2.5	121188	2	AC135605	Medicago
219	25	2.5	1940	6	173247	173247 Sequence 3	292	25	2.5	121488	8	AC137554	Medicago
220	25	2.5	1954	5	BC063984	BC063984 Danio rer	293	25	2.5	124770	2	AC146992	Lytechinu
221	25	2.5	1961	10	BC018539	BC018539 Mus muscu	294	25	2.5	125623	3	AC115599	Dictyoste
222	25	2.5	1967	10	BC005738	BC005738 Mus muscu	295	25	2.5	125736	2	BC323795	Danio rer
223	25	2.5	1973	5	AF378701	AF378701 Anas plat	296	25	2.5	126045	8	T3E15	Arabidops
224	25	2.5	1981	6	BD270074	BD270074 Secreted	297	25	2.5	126345	2	BC324229	Danio rer
225	25	2.5	2005	9	HSM801586	AL136613 Homo sapi	298	25	2.5	131707	5	BC247948	Zebrafish
226	25	2.5	2050	9	BC031567	BC031567 Homo sapi	299	25	2.5	132254	3	AC116330	Dictyoste
227	25	2.5	2112	3	AY069331	AY069331 Drosophi	300	25	2.5	134615	9	AC129576	Mus muscu
228	25	2.5	2149	6	AX018825	AX018825 Sequence	301	25	2.5	135506	9	AC009950	Homo sapi
229	25	2.5	2149	6	BD134935	BD134935 Human cys	302	25	2.5	137625	9	AC104663	Homo sapi
230	25	2.5	2174	5	BC064233	BC064233 Silurana	303	25	2.5	144041	8	AC135102	Medicago
231	25	2.5	2325	9	AB070171	AB070171 Macaca fa	304	25	2.5	146386	8	AC138130	Medicago
232	25	2.5	2369	10	RNGP56	X99338 R. norvegicu	305	25	2.5	146570	3	AC117072	Dictyoste
233	25	2.5	2562	3	AF102263	AF102263 Helicover	306	25	2.5	147889	2	AC018534	Homo sapi
234	25	2.5	2689	5	AB026130	AB026130 Cyprinus	307	25	2.5	148415	9	AC016670	Homo sapi
235	25	2.5	2722	9	BC047733	BC047733 Homo sapi	308	25	2.5	149768	2	AC016239	Homo sapi
236	25	2.5	2737	10	BC006676	BC006676 Mus muscu	309	25	2.5	150601	9	AC117426	Homo sapi
237	25	2.5	2749	9	AF146344	AF146344 Mus muscu	310	25	2.5	150628	10	AC133213	Mus muscu
238	25	2.5	2879	9	AF136972	AF136972 Homo sapi	311	25	2.5	151094	2	AC091797	Felis cat
239	25	2.5	2996	6	E17367	E17367 Oryza sativ	312	25	2.5	152409	2	AC091797	Felis cat
240	25	2.5	2996	6	E30255	E30255 Disease-res	313	25	2.5	152409	2	AC091797	Felis cat
241	25	2.5	2996	6	E30255	E30255 Disease-res	314	25	2.5	152409	2	AC091797	Felis cat
242	25	2.5	2996	6	E33921	E33921 Method for	315	25	2.5	154071	3	AC115598	Dictyoste
243	25	2.5	2996	6	E33933	E33933 Method for	316	25	2.5	154071	3	AC115598	Dictyoste
244	25	2.5	3110	9	HSM803101	AL173794 Homo sapi	317	25	2.5	160863	5	AL127955	Mus muscu
245	25	2.5	3389	9	AK027071	AK027071 Homo sapi	318	25	2.5	163866	10	AL929590	Zebrafish
246	25	2.5	3479	9	HSM807707	EX647561 Homo sapi	319	25	2.5	164900	2	EX571776	Danio rer
247	25	2.5	3533	3	CEL276018	AU276018 Caenorhab	320	25	2.5	165277	5	EX571776	Danio rer
248	25	2.5	3636	3	AY119446	AY119446 Drosophi	321	25	2.5	165373	2	EX990611	Danio rer
249	25	2.5	4116	5	AF406649	AF406649 Squallu a	322	25	2.5	166516	2	AC135510	Mus muscu
250	25	2.5	4134	6	AR182343	AR182343 Sequence	323	25	2.5	166516	2	AC135510	Mus muscu
251	25	2.5	4134	6	AR236221	AR236221 Sequence	324	25	2.5	169794	2	AC004688	Plasmodiu
252	25	2.5	4134	6	AR243543	AR243543 Sequence	325	25	2.5	171032	2	AC091761	Felis cat
253	25	2.5	4134	6	AR254415	AR254415 Sequence	326	25	2.5	171955	2	AL954354	Mus muscu
254	25	2.5	4134	6	AR321738	AR321738 Sequence	327	25	2.5	172493	2	AC146888	Bos tauru
255	25	2.5	4134	6	AR411424	AR411424 Sequence	328	25	2.5	174494	10	EX247953	Human DNA
256	25	2.5	4134	6	AR432994	AR432994 Sequence	329	25	2.5	175010	2	EX247953	Human DNA
257	25	2.5	4134	6	AX417770	AX417770 Sequence	330	25	2.5	175010	2	EX247953	Human DNA
258	25	2.5	4134	6	AX449101	AX449101 Sequence	331	25	2.5	175932	5	AL845359	Zebrafish
259	25	2.5	4134	6	AX743965	AX743965 Sequence	332	25	2.5	176038	9	EX284634	Mouse DNA
260	25	2.5	5273	9	HSM807780	EX647634 Homo sapi	333	25	2.5	176713	9	AP000751	Homo sapi
261	25	2.5	5708	10	BC054808	BC054808 Mus muscu	334	25	2.5	181515	10	AC127234	Mus muscu
262	25	2.5	9765	3	AY160106	AY160106 Dictyoste	335	25	2.5	182752	2	EX510936	Danio rer
263	25	2.5	14603	3	AC116959	AC116959 Dictyoste	336	25	2.5	182871	3	AC117176	Dictyoste
264	25	2.5	25769	3	AC115610	AC115610 Dictyoste	337	25	2.5	184831	2	AC016030	Homo sapi
265	25	2.5	29150	3	AC115683	AC115683 Dictyoste	338	25	2.5	185472	2	AC137513	Mus muscu
266	25	2.5	29176	8	AP001312	AP001312 Arabidops	339	25	2.5	187081	10	AC124421	Mus muscu
267	25	2.5	29176	8	AP001312	AP001312 Arabidops	340	25	2.5	191607	9	AL137186	Human DNA
268	25	2.5	77289	2	AC067975	AC067975 Homo sapi	341	25	2.5	191607	9	AL137186	Human DNA
269	25	2.5	81954	10	AL731562	AL731562 Mouse DNA	342	25	2.5	191635	10	EX119996	Mouse DNA
270	25	2.5	83552	9	AL157759	AL157759 Human DNA	343	25	2.5	191712	2	EX119996	Mouse DNA
271	25	2.5	88549	3	AC116979	AC116979 Dictyoste	344	25	2.5	191931	2	AP001958	Homo sapi
272	25	2.5	90596	8	T15B16	AF104919 Arabidops	345	25	2.5	192913	2	AP001958	Homo sapi
273	25	2.5	109027	10	AL732566	AL732566 Mouse DNA	346	25	2.5	195339	2	AC124707	Mus muscu
274	25	2.5	110000	2	PFMAL13_04	Continuation (5 of	347	25	2.5	196149	2	AC004709	Plasmodiu
275	25	2.5	110000	2	PFMAL13_07	Continuation (8 of	348	25	2.5	197064	8	ATCHRIV18	Arabidops
276	25	2.5	110000	2	PFMAL13_12	Continuation (13 o	349	25	2.5	198697	9	ATCHRIV4	Arabidops
277	25	2.5	110000	2	PFMAL13_13	Continuation (14 o	350	25	2.5	200182	8	ATCHRIV4	Arabidops
278	25	2.5	110000	2	PFMAL6PI_10	Continuation (11 o	351	25	2.5	202487	2	AC138318	Mus muscu
279	25	2.5	110000	2	PFMAL6PI_11	Continuation (12 o	352	25	2.5	205136	2	AC129583	Mus muscu
280	25	2.5	110000	2	PFMAL6PI_11	Continuation (12 o	353	25	2.5	205429	2	AC005506	Plasmodiu
281	25	2.5	110000	2	PFMAL7PI_06	Continuation (7 of	354	25	2.5	205429	2	AC141957	Rattus no
282	25	2.5	110000	2	PFMAL7PI_07	Continuation (8 of	355	25	2.5	208491	2	EX324225	Danio rer
283	25	2.5	110000	3	PFMAL8PI_05	Continuation (6 of	356	25	2.5	209037	2	AC134319	Fan troli
284	25	2.5	110000	3	AC116957_1	Continuation (2 of	357	25	2.5	211442	2	EX322617	Danio rer
285	25	2.5	110000	3	AC116957_2	Continuation (3 of	358	25	2.5	212712	2	AC063940	Homo sapi

358	25	2.5	213604	2	AC146006	AC146006 Pan trogl	431	24	2.4	608	5	AV138880	AV138880 Crocodylu
359	25	2.5	218112	2	AC140406	AC140406 Mus muscu	c 432	24	2.4	626	11	BV037178	BV037178 S20856749
360	25	2.5	218112	2	AC140406	AC140406 Mus muscu	433	24	2.4	651	3	AY060645	AY060645 Drosophil
361	25	2.5	222337	2	AC140368	AC140368 Mus muscu	434	24	2.4	651	10	BC018321	BC018321 Mus muscu
362	25	2.5	222887	2	AC015681	AC015681 Homo sapi	435	24	2.4	652	3	AF207542	AF207542 Drosophil
363	25	2.5	224370	2	AC097049	AC097049 Rattus no	436	24	2.4	657	9	BC061632	BC061632 Homo sapi
364	25	2.5	226006	10	AL603907	AL603907 Mouse DNA	437	24	2.4	662	9	HS0809205	BS649054 Homo sapi
365	25	2.5	227741	10	AC126071	AC126071 Rattus no	438	24	2.4	669	5	AY138894	AY138894 Crocodylu
366	25	2.5	237320	2	AC141339	AC141339 Rattus no	439	24	2.4	669	5	AY138894	AL049466 Homo sapi
367	25	2.5	240049	2	AC129660	AC129660 Rattus no	440	24	2.4	677	9	BC018211	BC018211 Homo sapi
368	25	2.5	242408	5	EX469926	EX469926 Zebrafish	441	24	2.4	680	5	AY138893	AY138893 Crocodylu
369	25	2.5	243954	10	AL669845	AL669845 Mouse DNA	442	24	2.4	685	6	AX406856	AX406856 Sequence
370	25	2.5	247150	2	AC135416	AC135416 Medicago	c 443	24	2.4	690	8	GMU38424	U38424 Glycine max
371	25	2.5	247527	2	AC107443	AC107443 Rattus no	444	24	2.4	716	5	AY138876	AY138876 Crocodylu
372	25	2.5	250195	3	AE014831	AE014831 Plasmodiu	445	24	2.4	716	10	BC028492	BC028492 Mus muscu
373	25	2.5	250748	2	AC094505	AC094505 Rattus no	446	24	2.4	722	9	BC062667	BC062667 Homo sapi
374	25	2.5	251448	3	AE014819	AE014819 Plasmodiu	447	24	2.4	723	9	HS0808728	EX468577 Homo sapi
375	25	2.5	252650	3	AE014847	AE014847 Plasmodiu	448	24	2.4	733	5	AY138891	AY138891 Crocodylu
376	25	2.5	253132	3	AE014846	AE014846 Plasmodiu	449	24	2.4	749	9	HS0420433	AJ420433 Homo sapi
377	25	2.5	254202	2	AC126506	AC126506 Rattus no	450	24	2.4	750	6	AX781131	AX781131 Sequence
378	25	2.5	254436	3	AE014827	AE014827 Plasmodiu	451	24	2.4	765	6	BD260633	BD260633 49 human
379	25	2.5	257109	3	AC115577	AC115577 Dictyoste	452	24	2.4	772	9	HS0802528	AL162009 Homo sapi
380	25	2.5	259289	2	AC096268	AC096268 Rattus no	453	24	2.4	792	10	BC048482	BC048482 Mus muscu
381	25	2.5	260277	2	AC114063	AC114063 Rattus no	454	24	2.4	796	10	BC038517	BC038517 Mus muscu
382	25	2.5	261553	2	AC137757	AC137757 Mus muscu	c 455	24	2.4	801	10	BC049657	BC049657 Mus muscu
383	25	2.5	272112	2	AC127940	AC127940 Rattus no	c 456	24	2.4	802	6	BD018631	BD018631 Novel gen
384	25	2.5	281723	3	PF0329359	AL929359 Plasmodiu	c 457	24	2.4	802	6	BD098569	BD098569 Novel gen
385	25	2.5	293431	2	PF04113P4	AL049181 Plasmodiu	458	24	2.4	807	8	NTA005899	AJ005899 Nicotiana
386	25	2.5	293962	2	AC112303	AC112303 Rattus no	459	24	2.4	817	6	BD215985	BD215985 Novel hum
387	25	2.5	306299	2	AC095803	AC095803 Rattus no	460	24	2.4	822	8	AF325718	AF325718 Pennisetu
388	25	2.5	333321	3	AC116986	AC116986 Dictyoste	461	24	2.4	834	9	BC015821	BC015821 Homo sapi
389	25	2.5	335050	3	PF0329356	AL929356 Plasmodiu	462	24	2.4	850	8	AF371268	AF371268 Zea mays
390	25	2.5	346257	2	AC114014	AC114014 Rattus no	463	24	2.4	852	3	AY246429	AY246429 Caenorhab
391	25	2.5	347888	2	AC125166	AC125166 Mus muscu	464	24	2.4	910	10	BC061146	BC061146 Mus muscu
392	24	2.4	47	6	BD234055	BD234055 DNA/prote	465	24	2.4	923	3	AF033913	AF033913 Ctenoceph
393	24	2.4	47	6	BD234061	BD234061 DNA/prote	466	24	2.4	923	6	AR125408	AR125408 Sequence
394	24	2.4	47	6	BD217378	BD217378 Sequence	467	24	2.4	923	6	AR144680	AR144680 Sequence
395	24	2.4	47	6	AR222450	AR222450 Sequence	468	24	2.4	923	6	AR214314	AR214314 Sequence
396	24	2.4	64	6	I18658	I18658 Sequence 10	469	24	2.4	937	10	BC022611	BC022611 Flea prot
397	24	2.4	93	6	E10247	E10247 Synthetic D	470	24	2.4	937	10	BC018362	BC018362 Mus muscu
398	24	2.4	101	6	E10248	E10248 Synthetic D	471	24	2.4	945	10	BC061019	BC061019 Mus muscu
399	24	2.4	121	6	AX324455	AX324455 Sequence	472	24	2.4	948	5	AY040528	AY040528 Gallus ga
400	24	2.4	121	6	AX324456	AX324456 Sequence	473	24	2.4	1004	6	AX247641	AX247641 Sequence
401	24	2.4	121	6	AX324483	AX324483 Sequence	474	24	2.4	1012	10	BC004052	BC004052 Mus muscu
402	24	2.4	121	6	AX324484	AX324484 Sequence	475	24	2.4	1030	8	AY227636	AY227636 Arabidops
403	24	2.4	121	6	AX324487	AX324487 Sequence	476	24	2.4	1053	10	BC052053	BC052053 Mus muscu
404	24	2.4	121	6	AX324488	AX324488 Sequence	477	24	2.4	1061	8	AF077760	AF077760 Oryza sat
405	24	2.4	121	6	AX324491	AX324491 Sequence	478	24	2.4	1065	3	AF429951	AF429951 Plasmodiu
406	24	2.4	121	6	AX324492	AX324492 Sequence	479	24	2.4	1068	9	BC035243	BC035243 Homo sapi
407	24	2.4	121	6	AX324495	AX324495 Sequence	480	24	2.4	1074	10	BC005740	BC005740 Mus muscu
408	24	2.4	121	6	AX324496	AX324496 Sequence	481	24	2.4	1084	8	AB003323	AB003323 Oryza sat
409	24	2.4	169	6	AX136221	AX136221 Sequence	482	24	2.4	1084	8	GSU50845	AJ250845 Gaidaria
410	24	2.4	189	6	AX208855	AX208855 Sequence	483	24	2.4	1088	9	BC010944	BC010944 Homo sapi
411	24	2.4	253	3	AK114512	AK114512 Ciona int	484	24	2.4	1093	6	BD269781	BD269781 50 human
412	24	2.4	317	9	AK000656	AK000656 Homo sapi	485	24	2.4	1101	9	BC006305	BC006305 Homo sapi
413	24	2.4	338	9	AB028624	AB028624 Homo sapi	486	24	2.4	1106	3	DJYBOX	X99748 D. japonica
414	24	2.4	374	6	AX198829	AX198829 Sequence	487	24	2.4	1109	5	AF460215	AF460215 Crocodylu
415	24	2.4	374	6	AX209356	AX209356 Sequence	488	24	2.4	1115	5	AF460212	AF460212 Crocodylu
416	24	2.4	414	9	HS0800130	AL050273 Homo sapi	489	24	2.4	1120	9	BC004117	BC004117 Homo sapi
417	24	2.4	431	3	AF483662	AF483662 Ixodes sc	490	24	2.4	1125	3	AY118732	AY118732 Drosophil
418	24	2.4	448	6	AX042185	AX042185 Sequence	491	24	2.4	1129	9	BC032788	BC032788 Homo sapi
419	24	2.4	465	6	AX408696	AX408696 Sequence	492	24	2.4	1133	6	AR225004	AR225004 Sequence
420	24	2.4	466	11	G21883	G21883 Human STS	493	24	2.4	1133	6	AF236370	AF236370 Zea mays
421	24	2.4	474	6	AL4236	AL4236 D5 anonymou	494	24	2.4	1143	5	AF198357	AF198357 Anguilla
422	24	2.4	478	8	GMU47406	U47406 Glycine max	495	24	2.4	1150	9	BC005042	BC005042 Homo sapi
423	24	2.4	501	10	BC019810	BC019810 Mus muscu	496	24	2.4	1161	5	AF460211	AF460211 Crocodylu
424	24	2.4	506	3	AF072331	AF072331 Schistos	497	24	2.4	1174	9	BC009797	BC009797 Homo sapi
425	24	2.4	521	6	AX381487	AX381487 Sequence	498	24	2.4	1186	9	BC014339	BC014339 Homo sapi
426	24	2.4	530	9	BC022858	BC022858 Homo sapi	499	24	2.4	1191	8	AF261141	AF261141 Lycopersi
427	24	2.4	578	8	AY299269	AY299269 Arabidops	500	24	2.4	1196	8	GNI32217	AJ132217 Gnetum gn
428	24	2.4	595	6	BD229601	BD229601 Human gen	501	24	2.4	1201	10	AF223416	AF223416 Mus muscu
429	24	2.4	604	5	AY138892	AY138892 Crocodylu	502	24	2.4	1205	9	BC011653	BC011653 Homo sapi
430	24	2.4	604	8	BT009360	BT009360 Triticum	503	24	2.4	1205	9	BC044945	BC044945 Homo sapi

504	24	2.4	1210	8	AK069317	AK069317 Oryza sat	577	24	2.4	1872	8	AF315733	AF315733 Arabidops
505	24	2.4	1213	10	AB016226	AB016226 Mus muscu	578	24	2.4	1876	10	MUSIGU1	M15555 Mouse Ig ac
506	24	2.4	1217	3	AF520473	AF520473 Branchios	579	24	2.4	1889	9	AF202889	AF202889 Homo sapi
507	24	2.4	1225	10	BC010797	BC010797 Mus muscu	580	24	2.4	1895	9	BC051752	BC051752 Homo sapi
508	24	2.4	1231	3	AF273806	AF273806 Caenorhab	581	24	2.4	1917	5	BC049324	BC049324 Danio rer
509	24	2.4	1234	3	AY069742	AY069742 Drosophil	582	24	2.4	1917	9	BC0009755	BC0009755 Homo sapi
510	24	2.4	1238	8	AF208051	AF208051 Arabidops	583	24	2.4	1921	6	AR438047	AR438047 Sequence
511	24	2.4	1238	8	BC017817	BC017817 Homo sapi	584	24	2.4	1921	6	BD192848	BD192848 Plant fat
512	24	2.4	1271	3	AY089282	AY089282 Drosophil	585	24	2.4	1924	10	BC024840	BC024840 Mus muscu
513	24	2.4	1281	10	BC024504	BC024504 Mus muscu	586	24	2.4	1925	10	BC055947	BC055947 Mus muscu
514	24	2.4	1287	3	BT009948	BT009948 Drosophil	587	24	2.4	1939	9	BC041927	BC041927 Homo sapi
515	24	2.4	1288	8	AF464903	AF464903 Triticum	588	24	2.4	1941	5	AF117343	AF117343 Fundulus
516	24	2.4	1291	8	CAR291816	AJ291816 Cicer ari	589	24	2.4	1942	10	BC046293	BC046293 Mus muscu
517	24	2.4	1303	6	E06716	E06716 cDNA encodi	590	24	2.4	1959	9	AK027180	AK027180 Homo sapi
518	24	2.4	1305	6	AR275654	AR275654 Sequence	591	24	2.4	1968	5	PPUGTWRN	W74116 P. platesea
519	24	2.4	1315	3	AY094690	AY094690 Drosophil	592	24	2.4	1971	6	AR078523	AR078523 Sequence
520	24	2.4	1323	6	BD091588	BD091588 Novel ser	593	24	2.4	1973	9	AB071133	AB071133 Macaca fa
521	24	2.4	1329	10	BC019428	BC019428 Mus muscu	594	24	2.4	2021	3	CEL345015	AJ345015 Caenorhab
522	24	2.4	1330	8	AY030360	AY030360 Oryza sat	595	24	2.4	2031	9	AK025437	AK025437 Homo sapi
523	24	2.4	1341	9	BC016737	BC016737 Homo sapi	596	24	2.4	2049	9	AK027165	AK027165 Homo sapi
524	24	2.4	1350	8	AY035056	AY035056 Arabidops	597	24	2.4	2082	5	BC044459	BC044459 Danio rer
525	24	2.4	1363	8	AF284038	AF284038 Cucurbita	598	24	2.4	2095	5	BC055677	BC055677 Danio rer
526	24	2.4	1369	5	BC053222	BC053222 Danio rer	599	24	2.4	2096	5	BC044459	BC044459 Danio rer
527	24	2.4	1369	8	AF399920	AF399920 Camellia	600	24	2.4	2098	9	AF060866	AF060866 Homo sapi
528	24	2.4	1397	5	BC054127	BC054127 Danio rer	601	24	2.4	2099	10	AY195875	AY195875 Mus muscu
529	24	2.4	1398	8	BT009141	BT009141 Triticum	602	24	2.4	2099	10	BC023090	BC023090 Mus muscu
530	24	2.4	1407	3	AY069115	AY069115 Drosophil	603	24	2.4	2111	9	BC003160	BC003160 Homo sapi
531	24	2.4	1409	9	BC031002	BC031002 Homo sapi	604	24	2.4	2125	6	I08142	I08142 Sequence 3
532	24	2.4	1430	6	BD234682	BD234682 TNP-assoc	605	24	2.4	2125	6	I09588	I09588 Sequence 7
533	24	2.4	1430	6	AR224049	AR224049 Sequence	606	24	2.4	2137	9	BC033678	BC033678 Homo sapi
534	24	2.4	1439	6	AR403758	AR403758 Sequence	607	24	2.4	2168	10	BC057992	BC057992 Mus muscu
535	24	2.4	1448	10	BC052344	BC052344 Mus muscu	608	24	2.4	2174	3	AK116693	AK116693 Ciona int
536	24	2.4	1462	9	AK024565	AK024565 Homo sapi	609	24	2.4	2179	10	MMTNF95	X57796 Mouse mRNa
537	24	2.4	1465	9	BC008042	BC008042 Homo sapi	610	24	2.4	2180	9	AF106697	AF106697 Homo sapi
538	24	2.4	1478	9	BC011645	BC011645 Homo sapi	611	24	2.4	2183	6	AK027227	AK027227 Homo sapi
539	24	2.4	1488	8	MTY10268	Y10268 M. truncatul	612	24	2.4	2185	6	BD249939	BD249939 50 human
540	24	2.4	1507	6	AR225245	AR225245 Sequence	613	24	2.4	2187	6	AR207293	AR207293 Sequence
541	24	2.4	1525	10	BC037042	BC037042 Mus muscu	614	24	2.4	2203	6	BD107867	BD107867 36 human
542	24	2.4	1536	10	BC011182	BC011182 Mus muscu	615	24	2.4	2209	3	AK114265	AK114265 Ciona int
543	24	2.4	1547	9	BC014022	BC014022 Homo sapi	616	24	2.4	2211	9	BC007443	BC007443 Homo sapi
544	24	2.4	1549	9	BSM808772	BX648621 Homo sapi	617	24	2.4	2217	6	AX827866	AX827866 Sequence
545	24	2.4	1550	5	BC059596	BC059596 Danio rer	618	24	2.4	2217	10	RNPOLIC	X70369 R.norvegicu
546	24	2.4	1562	8	BT0095156	AJ295156 Fragmite	619	24	2.4	2234	8	AF013979	AF013979 Oryza sat
547	24	2.4	1565	8	BT009560	BT009560 Triticum	620	24	2.4	2236	9	BC033633	BC033633 Homo sapi
548	24	2.4	1573	9	BC015481	BC015481 Homo sapi	621	24	2.4	2251	10	BC030879	BC030879 Mus muscu
549	24	2.4	1579	5	BC050174	BC050174 Danio rer	622	24	2.4	2253	9	HSN803406	AL832039 Homo sapi
550	24	2.4	1582	9	BC009933	BC009933 Homo sapi	623	24	2.4	2266	6	AB070028	AB070028 Macaca fa
551	24	2.4	1585	5	BC064156	BC064156 Silurana	624	24	2.4	2268	6	AX590640	AX590640 Sequence
552	24	2.4	1588	6	AE2526	AE2526 Sequence 31	625	24	2.4	2341	3	AF193553	BC036723 Homo sapi
553	24	2.4	1588	9	AF038172	AF038172 Homo sapi	626	24	2.4	2352	3	AF193553	AF193553 Drosophil
554	24	2.4	1600	9	BC035597	BC035597 Homo sapi	627	24	2.4	2353	9	HSN801942	BC060036 Mus muscu
555	24	2.4	1616	3	AF207536	AF207536 Drosophil	628	24	2.4	2365	10	BC060036	BC064418 Homo sapi
556	24	2.4	1619	9	BC018671	BC018671 Homo sapi	629	24	2.4	2421	9	BC064418	BC064418 Homo sapi
557	24	2.4	1624	6	AR165164	AR165164 Sequence	630	24	2.4	2421	10	BC061106	BC061106 Mus muscu
558	24	2.4	1631	10	AF393243	AF393243 Rattus no	631	24	2.4	2432	8	AF080436	AF080436 Oryza sat
559	24	2.4	1631	10	AY23297	AY23297 Mus muscu	632	24	2.4	2448	9	HSN801408	AL133551 Homo sapi
560	24	2.4	1646	9	AF035287	AF035287 Homo sapi	633	24	2.4	2459	10	AF187876	AF187876 Cavia por
561	24	2.4	1660	8	AY376878	AY376878 Malus x d	634	24	2.4	2463	9	BC020957	BC020957 Homo sapi
562	24	2.4	1663	8	AF058763	AF058763 Zea mays	635	24	2.4	2480	6	AX128511	AX128511 Sequence
563	24	2.4	1689	4	FCAN916	AJ009816 Felis cat	636	24	2.4	2501	9	BC000285	BC000285 Homo sapi
564	24	2.4	1702	6	AX073668	AX073668 Sequence	637	24	2.4	2508	5	AY204552	AY204552 Xenopus l
565	24	2.4	1731	8	AF405700	AF405700 Solanum t	638	24	2.4	2528	10	BC023296	BC023296 Mus muscu
566	24	2.4	1733	8	AF035252	AF035252 Glycine m	639	24	2.4	2546	9	PPYL6568	Y16668 Papio papio
567	24	2.4	1734	6	AR175261	AR175261 Sequence	640	24	2.4	2554	9	BC051855	BC051855 Homo sapi
568	24	2.4	1750	9	AF175767	AF175767 Homo sapi	641	24	2.4	2627	10	BC024887	BC024887 Mus muscu
569	24	2.4	1755	8	D86591	D86591 Arabidopsis	642	24	2.4	2639	9	BC014109	BC014109 Homo sapi
570	24	2.4	1757	9	BC002336	BC002336 Homo sapi	643	24	2.4	2654	3	DDIDG17A	M18106 Dictyostell
571	24	2.4	1760	6	BD275033	BD275033 50 Human	644	24	2.4	2700	6	AX794710	AX794710 Sequence
572	24	2.4	1776	5	BC055206	BC055206 Danio rer	645	24	2.4	2724	10	BC043057	BC043057 Mus muscu
573	24	2.4	1791	3	PX489522	AJ489522 Plutella	646	24	2.4	2731	9	BSM807275	BC007275 Homo sapi
574	24	2.4	1817	10	BC051174	BC051174 Mus muscu	647	24	2.4	2768	9	HSN804810	AL136842 Homo sapi
575	24	2.4	1843	9	BC021164	BC021164 Homo sapi	648	24	2.4	2775	5	PAPFOAT	Z970028 Pseudopleur
576	24	2.4	1865	10	BC018252	BC018252 Mus muscu	649	24	2.4	2775	10	AB041607	AB041607 Mus muscu

650	24	2.4	2827	3	TSP005937	AJ005937 Tealia sp	723	24	2.4	69562	2	AC101403	AC101403 Mus muscu
651	24	2.4	2857	10	BC031847	BC031847 Mus muscu	724	24	2.4	70571	2	AC145071	AC145071 Mus muscu
652	24	2.4	2873	10	BC052412	BC052412 Mus muscu	725	24	2.4	72957	2	AC025304	AC025304 Homo sapi
653	24	2.4	2899	9	AB050256	AB050256 Macaca fa	726	24	2.4	73575	10	AL645766	AL645766 Mouse DNA
654	24	2.4	2924	10	AF498039	AF498039 Rattus no	727	24	2.4	74841	10	AL806529	AL806529 Mouse DNA
655	24	2.4	3012	10	AF293383	AF293383 Rattus no	728	24	2.4	76066	9	AL162588	AL162588 Human DNA
656	24	2.4	3120	10	AB078879	AB078879 Rattus no	729	24	2.4	78756	2	PFMAL6P1_13	PFMAL6P1_13 Continuation (14 o
657	24	2.4	3213	6	BD192218	BD192218 Secrated	730	24	2.4	80019	8	ATF25E4	ATF25E4 Arabidops
658	24	2.4	3314	8	AB110951	AB110951 Delphinu	731	24	2.4	80725	9	AL137078	AL137078 Human DNA
659	24	2.4	3334	3	AY254474	AY254474 Dictyoste	732	24	2.4	83395	2	AC087137	AC087137 Mus muscu
660	24	2.4	3379	10	BC031531	BC031531 Mus muscu	733	24	2.4	84139	3	AC115684	AC115684 Dictyoste
661	24	2.4	3392	9	BC006541	BC006541 Homo sapi	734	24	2.4	83885	2	AC122729	AC122729 Medicago
662	24	2.4	3409	10	BC036148	BC036148 Mus muscu	735	24	2.4	84550	3	PFMAL1P2_3	PFMAL1P2_3 Continuation (4 of
663	24	2.4	3452	8	AF369909	AF369909 Arabidops	736	24	2.4	84554	8	AC123571	AC123571 Medicago
664	24	2.4	3465	10	BC042443	BC042443 Mus muscu	737	24	2.4	84816	5	BX324216	BX324216 Zebrafish
665	24	2.4	3493	10	BC053711	BC053711 Mus muscu	738	24	2.4	85916	3	AC117080	AC117080 Dictyoste
666	24	2.4	3520	9	BSM801234	BSM801234 Homo sapi	739	24	2.4	86811	9	AC018401	AC018401 Homo sapi
667	24	2.4	3634	9	BC040239	BC040239 Homo sapi	740	24	2.4	86945	2	AC002490	AC002490 Homo sapi
668	24	2.4	3666	9	BSM805473	BSM805473 Homo sapi	741	24	2.4	88947	2	AP005463	AP005463 Oryza sat
669	24	2.4	3916	9	BSM802233	BSM802233 Homo sapi	742	24	2.4	89389	8	AC140548	AC140548 Medicago
670	24	2.4	3919	9	HSEG11	V00508 Human gene	743	24	2.4	90220	9	HSJ734P14	HSJ734P14 Human DNA
671	24	2.4	3967	10	BC028248	BC028248 Mus muscu	744	24	2.4	90587	2	AC140671	AC140671 Medicago
672	24	2.4	4042	9	AF087142	AF087142 Homo sapi	745	24	2.4	91927	9	AC004771	AC004771 Homo sapi
673	24	2.4	4044	3	AY118635	AY118635 Drosophil	746	24	2.4	94510	9	HS39083	HS39083 Human DNA s
674	24	2.4	4074	6	AX305897	AX305897 Sequence	747	24	2.4	94645	9	AF225900	AF225900 Homo sapi
675	24	2.4	4074	10	MUSGABAX	M92378 Mus musculu	748	24	2.4	96433	3	DMEN519	DMEN519 Drosophil
676	24	2.4	4169	10	BC059080	BC059080 Mus muscu	749	24	2.4	101002	3	AY216936	AY216936 Plasmidiu
677	24	2.4	4174	8	BT004118	BT004118 Arabidops	750	24	2.4	101016	3	AY216937	AY216937 Plasmidiu
678	24	2.4	4230	3	AF465310	AF465310 Dictyoste	751	24	2.4	101095	3	AY216937	AY216937 Plasmidiu
679	24	2.4	4254	5	CHKESTP20	D82364 Gallus gall	752	24	2.4	101158	3	AY216938	AY216938 Plasmidiu
680	24	2.4	4297	9	EC038505	EC038505 Homo sapi	753	24	2.4	101167	9	HS3217	HS3217 Human DNA
681	24	2.4	4443	10	BC049788	BC049788 Mus muscu	754	24	2.4	101884	8	AC142224	AC142224 Medicago
682	24	2.4	4476	9	BC063501	BC063501 Homo sapi	755	24	2.4	103576	8	YUP8H12	YUP8H12 Arabidops
683	24	2.4	4662	10	BC060645	BC060645 Mus muscu	756	24	2.4	106260	9	AC005477	AC005477 Homo sapi
684	24	2.4	4724	9	BSM808698	BSM808698 Homo sapi	757	24	2.4	106267	2	AP000749	AP000749 Homo sapi
685	24	2.4	4778	10	BC043089	BC043089 Mus muscu	758	24	2.4	107650	9	AC108677	AC108677 Homo sapi
686	24	2.4	4812	10	BC058724	BC058724 Mus muscu	759	24	2.4	108028	8	AC135233	AC135233 Medicago
687	24	2.4	4842	8	AF424549	AF424549 Oryza sat	760	24	2.4	108240	2	AC146584	AC146584 Medicago
688	24	2.4	4988	10	BC051169	BC051169 Mus muscu	761	24	2.4	110000	9	HS523G1	HS523G1 Human DNA
689	24	2.4	5071	10	BC052464	BC052464 Mus muscu	762	24	2.4	110000	2	AC091449_1	AC091449_1 Continuation (2 of
690	24	2.4	5231	10	BC048170	BC048170 Mus muscu	763	24	2.4	110000	2	AC096457_0	AC096457_0 Rattus no
691	24	2.4	5686	9	BSM808430	BSM808430 Homo sapi	764	24	2.4	110000	2	AC096457_1	AC096457_1 Continuation (2 of
692	24	2.4	6372	3	DDICNPA	M23449 Dictyoselin	765	24	2.4	110000	2	AC102983_1	AC102983_1 Continuation (2 of
693	24	2.4	6582	6	AX481755	AX481755 Sequence	766	24	2.4	110000	2	AC105883_2	AC105883_2 Continuation (3 of
694	24	2.4	7860	9	BSM809154	BSM809154 Homo sapi	767	24	2.4	110000	2	AC120752_2	AC120752_2 Continuation (3 of
695	24	2.4	8059	2	AC087223	AC087223 Homo sapi	768	24	2.4	110000	2	AC123221_0	AC123221_0 Rattus no
696	24	2.4	9751	3	AF465309	AF465309 Dictyoste	769	24	2.4	110000	2	AL845451_0	AL845451_0 Mus muscu
697	24	2.4	10131	9	AB035192	AB035192 Homo sapi	770	24	2.4	110000	2	BSX10910_2	BSX10910_2 Continuation (3 of
698	24	2.4	10583	5	AB040746	AB040746 Carassius	771	24	2.4	110000	2	PFMAL13_09	PFMAL13_09 Continuation (10 o
699	24	2.4	11829	3	AE001376	AE001376 Plasmidiu	772	24	2.4	110000	2	PFMAL13_25	PFMAL13_25 Continuation (26 o
700	24	2.4	14855	10	AF187875	AF187875 Cavia por	773	24	2.4	110000	2	PFMAL13_26	PFMAL13_26 Continuation (27 o
701	24	2.4	17839	3	AE001384	AE001384 Plasmidiu	774	24	2.4	110000	2	PFMAL6P1_09	PFMAL6P1_09 Continuation (10 o
702	24	2.4	18011	6	AX344936	AX344936 Sequence	775	24	2.4	110000	2	PFMAL7P1_08	PFMAL7P1_08 Continuation (9 of
703	24	2.4	25994	4	AL732600	AL732600 Human DNA	776	24	2.4	110000	2	PFMAL8P1_03	PFMAL8P1_03 Continuation (4 of
704	24	2.4	32256	2	AL513169	AL513169 Homo sapi	777	24	2.4	110000	2	PFMAL8P1_05	PFMAL8P1_05 Continuation (6 of
705	24	2.4	33270	3	AC116921	AC116921 Dictyoste	778	24	2.4	110000	2	PFMAL8P1_07	PFMAL8P1_07 Continuation (8 of
706	24	2.4	33569	3	AC115685	AC115685 Dictyoste	779	24	2.4	110000	2	PFMAL8P1_09	PFMAL8P1_09 Continuation (10 o
707	24	2.4	36506	2	AC013220	AC013220 Drosophil	780	24	2.4	110000	10	AE008684_0	AE008684_0 Mus muscu
708	24	2.4	39459	2	AC018136	AC018136 Drosophil	781	24	2.4	110268	2	AC135465	AC135465 Medicago
709	24	2.4	44948	10	BSX71769	BSX71769 Mouse DNA	782	24	2.4	111882	3	AC115612	AC115612 Dictyoste
710	24	2.4	46441	9	AP003388	AP003388 Homo sapi	783	24	2.4	112389	2	AC073598	AC073598 Homo sapi
711	24	2.4	47736	3	AC004353	AC004353 Drosophil	784	24	2.4	112513	2	AC141825	AC141825 Apis mell
712	24	2.4	48500	10	AL772259	AL772259 Mouse DNA	785	24	2.4	113506	2	AC121243	AC121243 Medicago
713	24	2.4	53993	2	AC100666	AC100666 Mus muscu	786	24	2.4	113738	3	PFMAL3P4	PFMAL3P4 Mus muscu
714	24	2.4	55527	2	AC100278	AC100278 Mus muscu	787	24	2.4	113880	3	PFMAL3P4	PFMAL3P4 Plasmidiu
715	24	2.4	59030	2	AC087959	AC087959 Homo sapi	788	24	2.4	114142	8	AC127170	AC127170 Medicago
716	24	2.4	59130	2	AC118265	AC118265 Mus muscu	789	24	2.4	114226	2	AC004710	AC004710 Plasmidiu
717	24	2.4	60721	9	BSX31878	BSX31878 Human DNA	790	24	2.4	115496	2	AC146743	AC146743 Medicago
718	24	2.4	61210	9	AC011409	AC011409 Homo sapi	791	24	2.4	118777	10	AF163865	AF163865 Mouse DNA
719	24	2.4	67840	2	AC103375	AC103375 Mus muscu	792	24	2.4	119774	10	AL731705	AL731705 Mouse DNA
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721	24	2.4	68952	2	AC101387	AC101387 Mus muscu	794	24	2.4	120913	10	AL844545	AL844545 Mouse DNA
722	24	2.4	69303	9	AL357496	AL357496 Human DNA	795	24	2.4	121063	2	AC079482	AC079482 Mus muscu

796	24	2.4	121251	5	AL591593	AL591593 Zebrafish	C 869	24	2.4	153629	9	AC092325	AC092325 Homo sapi
797	24	2.4	122243	2	AC144931	AC144931 Zebrafish	C 870	24	2.4	153880	5	AL928800	AL928800 Zebrafish
C 798	24	2.4	123909	8	AC138451	AC138451 Medicago	871	24	2.4	153992	2	BX890560	BX890560 Danio rer
C 799	24	2.4	124169	2	AC146752	AC146752 Medicago	872	24	2.4	154273	10	AC127577	AC127577 Mus muscu
800	24	2.4	125346	2	AP004329	AP004329 Oryza sat	873	24	2.4	154484	10	AC121944	AC121944 Mus muscu
801	24	2.4	125479	9	BSJ244F24	BSJ244F24 Human DNA	C 874	24	2.4	155856	10	BSX72626	BSX72626 Mouse DNA
C 802	24	2.4	125764	3	AC008528	AC008528 Homo sapi	875	24	2.4	156016	2	AL808135	AL808135 Mouse DNA
C 803	24	2.4	125958	3	AC115592	AC115592 Dictyoste	876	24	2.4	156113	2	AC120352	AC120352 Mus muscu
C 804	24	2.4	125992	2	AC142222	AC142222 Medicago	877	24	2.4	156257	2	BSX11252	BSX11252 Danio rer
C 805	24	2.4	126122	2	AC144187	AC144187 Macaca mu	C 878	24	2.4	156461	2	AC021607	AC021607 Homo sapi
C 806	24	2.4	128503	9	AC090907	AC090907 Homo sapi	879	24	2.4	156630	2	AC145842	AC145842 Papio anu
807	24	2.4	129039	10	AL808113	AL808113 Mouse DNA	880	24	2.4	156830	2	AC027693	AC027693 Homo sapi
C 808	24	2.4	129169	2	AC032038	AC032038 Homo sapi	881	24	2.4	157167	2	AC118166	AC118166 Mus muscu
C 809	24	2.4	129263	9	AL360089	AL360089 Human DNA	882	24	2.4	157310	2	AC118166	AC118166 Mus muscu
C 810	24	2.4	129285	5	AC091726	AC091726 Gallus ga	883	24	2.4	157350	2	AC118166	AC118166 Mus muscu
811	24	2.4	129412	2	AC119892	AC119892 Mus muscu	C 884	24	2.4	157383	9	AC021607	AC021607 Homo sapi
C 812	24	2.4	132090	10	AC005402	AC005402 Mus muscu	885	24	2.4	157502	2	AC145842	AC145842 Papio anu
C 813	24	2.4	132573	9	AC015564	AC015564 Homo sapi	886	24	2.4	157701	2	AC058814	AC058814 Homo sapi
C 814	24	2.4	133400	2	AC134521	AC134521 Medicago	C 887	24	2.4	157860	9	AL391241	AL391241 Human DNA
C 815	24	2.4	133971	2	AC138464	AC138464 Medicago	888	24	2.4	158186	2	BSX890603	BSX890603 Danio rer
816	24	2.4	134680	9	AC015726	AC015726 Homo sapi	889	24	2.4	158202	2	AC119414	AC119414 Medicago
817	24	2.4	135658	8	AC141863	AC141863 Medicago	C 890	24	2.4	158279	2	AC145373	AC145373 Mus muscu
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819	24	2.4	136031	9	AL645568	AL645568 Human DNA	892	24	2.4	158438	9	AC068757	AC068757 Homo sapi
C 820	24	2.4	136088	9	AL139426	AL139426 Human DNA	893	24	2.4	158472	2	BSX21912	BSX21912 Danio rer
C 821	24	2.4	136240	3	AC117070	AC117070 Dictyoste	894	24	2.4	158548	3	PFMAL3P2	PFMAL3P2 Plasmodiu
822	24	2.4	136445	2	AC102346	AC102346 Mus muscu	895	24	2.4	158581	2	AC147528	AC147528 Otolomur
823	24	2.4	136470	2	AC145222	AC145222 Medicago	896	24	2.4	159114	2	AC132246	AC132246 Mus muscu
C 824	24	2.4	137333	5	AL935167	AL935167 Zebrafish	C 897	24	2.4	159602	9	CNS01DRH	CNS01DRH Human chr
C 825	24	2.4	137751	10	AC091452	AC091452 Mus muscu	898	24	2.4	159937	10	AL845504	AL845504 Mouse DNA
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C 828	24	2.4	140771	10	AL591611	AL591611 Mouse DNA	C 901	24	2.4	160586	2	AC126319	AC126319 Mus muscu
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C 830	24	2.4	142711	10	AC121863	AC121863 Mus muscu	C 903	24	2.4	160970	9	AC010138	AC010138 Homo sapi
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833	24	2.4	143035	9	AC010082	AC010082 Homo sapi	906	24	2.4	161169	10	BX470101	BX470101 Mouse DNA
834	24	2.4	143428	9	AL162587	AL162587 Human DNA	C 907	24	2.4	161871	9	AP002806	AP002806 Homo sapi
835	24	2.4	144376	10	AC133088	AC133088 Mus muscu	908	24	2.4	161973	10	AC126680	AC126680 Mus muscu
836	24	2.4	144545	10	AC132102	AC132102 Mus muscu	909	24	2.4	161976	2	AC012415	AC012415 Homo sapi
C 837	24	2.4	144666	9	AL160287	AL160287 Human DNA	C 910	24	2.4	162045	10	AC125452	AC125452 Mus muscu
C 838	24	2.4	145215	2	AC102891	AC102891 Mus muscu	911	24	2.4	162215	9	AC004896	AC004896 Homo sapi
839	24	2.4	145391	2	AC131186	AC131186 Mus muscu	C 912	24	2.4	162242	2	AC090803	AC090803 Homo sapi
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841	24	2.4	146734	10	AL590415	AL590415 Mouse DNA	C 914	24	2.4	162814	10	AC132594	AC132594 Mus muscu
C 842	24	2.4	146937	2	AC112817	AC112817 Rattus no	C 915	24	2.4	162858	10	AC132598	AC132598 Mus muscu
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844	24	2.4	147367	2	AC073966	AC073966 Homo sapi	C 917	24	2.4	163668	2	BSX119984	BSX119984 Danio rer
C 845	24	2.4	147584	9	AC013829	AC013829 Homo sapi	C 918	24	2.4	163918	9	CNS01DRH	CNS01DRH Human chr
C 846	24	2.4	147712	2	AC117939	AC117939 Caris fam	C 919	24	2.4	163926	5	BSX000481	BSX000481 Zebrafish
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C 849	24	2.4	148930	9	AC073316	AC073316 Homo sapi	C 922	24	2.4	164470	9	AC012346	AC012346 Homo sapi
C 850	24	2.4	149003	2	BSX37320	BSX37320 Danio rer	C 923	24	2.4	164539	10	AC122738	AC122738 Medicago
C 851	24	2.4	149047	10	AC134564	AC134564 Mus muscu	924	24	2.4	164663	2	AC138580	AC138580 Mouse DNA
852	24	2.4	149870	9	AC024579	AC024579 Homo sapi	C 925	24	2.4	164991	10	AL732429	AL732429 Mouse DNA
853	24	2.4	150443	2	BSX284672	BSX284672 Danio rer	926	24	2.4	165510	10	AL833788	AL833788 Mouse DNA
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C 856	24	2.4	151503	2	AC141833	AC141833 Apis mell	C 929	24	2.4	165554	2	AC069083	AC069083 Homo sapi
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C 858	24	2.4	151646	9	AC098964	AC098964 Homo sapi	C 931	24	2.4	165804	2	AC147454	AC147454 Didelphis
C 859	24	2.4	151669	10	AC114560	AC114560 Mus muscu	C 932	24	2.4	165881	2	AC137732	AC137732 Rattus no
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C 861	24	2.4	152039	9	AC097489	AC097489 Homo sapi	C 934	24	2.4	167208	2	AC034190	AC034190 Homo sapi
C 862	24	2.4	152454	2	AC142094	AC142094 Medicago	C 935	24	2.4	167554	2	AC116782	AC116782 Mus muscu
863	24	2.4	152632	2	AC116837	AC116837 Mus muscu	C 936	24	2.4	167633	2	AC116782	AC116782 Mus muscu
C 864	24	2.4	152632	2	AC116837	AC116837 Mus muscu	C 937	24	2.4	167744	2	AC130653	AC130653 Medicago
C 865	24	2.4	153089	9	AC146510	AC146510 Pan trogl	C 938	24	2.4	167998	10	AC124418	AC124418 Mus muscu
C 866	24	2.4	153191	10	AC125527	AC125527 Mus muscu	939	24	2.4	168181	10	AC124458	AC124458 Mus muscu
C 867	24	2.4	153232	5	AL928821	AL928821 Zebrafish	940	24	2.4	168346	2	AC036227	AC036227 Homo sapi
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C 942 24 2.4 168354 10 AC124382
 C 943 24 2.4 168396 10 AC129774
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 945 24 2.4 168620 2 AC121544
 946 24 2.4 169207 9 AC007490
 947 24 2.4 169424 2 AL929203
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 C 950 24 2.4 169546 2 AC004157
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 C 954 24 2.4 170666 10 AC134392
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 957 24 2.4 171254 10 AL845294
 958 24 2.4 171309 9 AC012146
 959 24 2.4 171477 2 AC102467
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 C 997 24 2.4 178699 9 AL732500
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 999 24 2.4 179007 2 AC012275
 1000 24 2.4 179063 9 AL928711

ALIGNMENTS

RESULT 1
 MDO251116
 LOCUS Malus domestica mRNA for B-type MADS box protein (mads13 gene).
 DEFINITION AJ251116 1102 bp mRNA linear PLN 16-NOV-2001
 ACCESSION AJ251116
 VERSION AJ251116.1 GI:16973293
 KEYWORDS B-type MADS box protein; mads13 gene.
 SOURCE Malus x domestica (apple tree)
 ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 1
 Vosman,B. and Smulders,M.J.M.
 Isolation of apple B- and C-type MADS box genes from vegetative
 tissue
 Unpublished
 2 (bases 1 to 1102)
 van der Linden,C.G.
 Direct Submission
 Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic
 Diversity, CPRO Wageningen University & Research Centre, PO Box 16,
 Wageningen, 6700 AA, NETHERLANDS
 Location/Qualifiers
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 RGNMLHGYFDOEAAGDPQGYEDNEGDYESALASNGANNLYTFHLHRLNHLHGSS
 LGSSITHLHLRLA"
 ORIGIN
 Query Match 81.6%; Score 801; DB 8; Length 1102;
 Best Local Similarity 93.7%; Pred. No. 0;
 Matches 951; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 DB 80 GGGAGATTGAAATCAAGCTGATCGAAACACAGACCAAGGAGGTCACCTACTCCAAG 139
 QY 70 AGAAGAAATGGATCTTCAAGAGGCTCAGAGGTCACCGTCTCTGTGTGACCAAGGTC 129
 DB 140 AGAAGAAATGGATCTTCAAGAGGCTCAGAGGTCACCGTCTCTGTGTGACCAAGGTC 199
 QY 130 TCCCTCATTTGCTCTCCACACCTAATAAATGACAGGATATATCAGCCCTACCACTACG 189
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 QY 190 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
 DB 260 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319
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 DB 320 GAGAGTCGATGAAGACACCTCTGGAAGTTCGAAGATCAACATAGCTGAGGAGGAG 379
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 DB 380 GAGATCAGGAGGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAGCTGGCTTCT 439
 QY 370 CTTGACCATGAGTGCAGTCTTCTTGGATGCCATAGCTCAAGAGGATCAAGTGTGATC 429
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980 TGTATAATTAATCTTCTATCTAT 1033

RESULT 2
AB081094
LOCUS
DEFINITION
AB081094
ACCESSION
AB081094.1
VERSION
KEYWORDS
SOURCE
ORGANISM

Malus x domestica (apple tree)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE
1
Matsumoto, S., Ohtsubo, T. and Soejima, J.
Cloning and sequencing of apple MADS-box genes 'MdPI', 'MdTM6' and
'MdMADS13',
Unpublished

JOURNAL
REFERENCE
2
Ohtsubo, T. and Matsumoto, S.
Direct Submission
Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,
Gifu 501-1193, Japan (E-mail: shmatsum@gifu-u.ac.jp,
Tel: 81-58-293-2257, Fax: 81-58-293-2207)

JOURNAL
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3
Ohtsubo, T. and Matsumoto, S.
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JOURNAL
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JOURNAL
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10
Ohtsubo, T. and Matsumoto, S.
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JOURNAL
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JOURNAL
REFERENCE
12
Ohtsubo, T. and Matsumoto, S.
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JOURNAL
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14
Ohtsubo, T. and Matsumoto, S.
Direct Submission
Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
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JOURNAL
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15
Ohtsubo, T. and Matsumoto, S.
Direct Submission
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JOURNAL
REFERENCE
16
Ohtsubo, T. and Matsumoto, S.
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Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,
Gifu 501-1193, Japan (E-mail: shmatsum@gifu-u.ac.jp,
Tel: 81-58-293-2257, Fax: 81-58-293-2207)

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QY 530 ATCCACAGTATGTTTATGAGGCAATGAGGAGACTACGAATCTGCATTTGCAATGTC 589
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QY 590 ATGGGCGGAATAAATGTTGACACTTTCCACCTCCACCACTTCCACCTCCACCACT 649
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QY 650 GTCGCTCGGCTCCCTCACTTACTCATCTGCAGATCTCGGCTTCTGATCGTATCTG 709
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QY 710 AGATATGATTAATCACTCACTAAGTTATATATTAAGTCACTTATACTGCTTTTGTCT 769
DB 252 AGATATGATTAATCACTCACTAAGTTATATATTAAGTCACTTATACTGCTTTTGTCT 311
QY 770 AAGTGTTCCTTGGTGACTATCTTTAGCAAGAGTAGACTTTGACATCTCTGAAAC 829
DB 312 AAGTGTTCCTTGGTGACTATCTTTAGCAAGAGTAGACTTTGACATCTCTGAAAC 371
QY 830 AGATGATTAATGATGCTGCTGTTTAAATCAATGATAGCACTAAAAAATCCGCGCC 889
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DB 432 TTGTTGCTTGTGGGTTTGT 450

RESULT 3

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LOCUS
DEFINITION
AB081093
ACCESSION
AB081093.1
VERSION
KEYWORDS
SOURCE
ORGANISM

Malus x domestica (apple tree)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

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1
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Unpublished

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Gifu 501-1193, Japan (E-mail: shmatsum@gifu-u.ac.jp,
Tel: 81-58-293-2257, Fax: 81-58-293-2207)

FEATURES

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ACCESSION	AB055966	
VERSION	AB055966.1 GI:15216292	
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SOURCE	Rosa rugosa	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.	
REFERENCE	1 Kitahara,K., Hirai,S., Fukui,H. and Matsumoto,S. Rose MADS-box genes 'MASAKO BP and B3' homologous to class B floral identity genes	
AUTHORS	Plant Sci. 161, 549-557 (2001)	
TITLE	2 (bases 1 to 1014)	
JOURNAL	Matsumoto,S., Hirai,S. and Kitahara,K.	
REFERENCE	Submitted (19-FEB-2001) Shogo Matsumoto, Gifu University, Department of Biology, Faculty of Education, 1-1, Yangigido, Gifu, Gifu 501-1193, Japan. [E-mail:smatsumo@gifu-u.ac.jp, Tel:81-58-293-2257, Fax:81-58-293-2207]	
AUTHORS	Location/Qualifiers	
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5690 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 5719

RESULT 6
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DEFINITION Mouse DNA sequence from clone RP23-84E1 on chromosome 2, complete
sequence.
ACCESSION AL935278
VERSION AL935278.7 GI:27652829
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 183353)
JOURNAL Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Phillimore, B.
Direct Submission

Submitted (09-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Jan 11, 2003 this sequence version replaced gi:27497292.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-84E1 is
from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6.

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FEATURES
source

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Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 166463 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 166434

RESULT 7
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DEFINITION Nicotiana tabacum mRNA for carbamoyl phosphate synthase small
subunit.
ACCESSION AJ319873
VERSION AJ319873.1 GI:21535792
KEYWORDS carbamoyl phosphate synthase small subunit.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE 1 (bases 1 to 1698)
JOURNAL Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
AUTHORS asterids; lamids; Solanales; Solanaceae; Nicotiana.
Zrenner, R., Schroeder, M. and Giermann, N.
Molecular analysis of de novo pyrimidine synthesis in plants
Unpublished
REFERENCE 2 (bases 1 to 1698)
AUTHORS Zrenner, R.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Zrenner R., Ruprecht-Karls-Universitaet
Heidelberg, Botanisches Institut, INF 360, 69120 Heidelberg,
GERMANY

Location/Qualifiers
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FEATURES
source

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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
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Db 1670 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 1698

RESULT 8
ATHPRPHA
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ACCESSION M96732
VERSION M96732.1 GI:166820
KEYWORDS protein phosphatase.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE 1 (bases 1 to 1255)
JOURNAL Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
AUTHORS rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Zrenner, R., Schroeder, M. and Giermann, N.
Molecular analysis of de novo pyrimidine synthesis in plants
Unpublished
REFERENCE 2 (bases 1 to 1698)
AUTHORS Zrenner, R.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Zrenner R., Ruprecht-Karls-Universitaet
Heidelberg, Botanisches Institut, INF 360, 69120 Heidelberg,
GERMANY

Location/Qualifiers
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FEATURES
source

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AUTHORS      1 (bases 1 to 1256)
              Arino,J., Perez-Callejon,E., Cunillera,N., Camps,M., Posas,F. and
              Ferrer,A.
TITLE        Protein phosphatases in higher plants: multiplicity of type 2A
              phosphatases in Arabidopsis thaliana
JOURNAL      Plant Mol. Biol. 21 (3), 475-485 (1993)
MEDLINE      93184204
PUBMED       8382968
COMMENT      Original source text: Arabidopsis thaliana (library: lambda GT10)
              young adult in flowering stage whole plant (including root) cDNA to
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Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 1192 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 1219

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LOCUS       ATRXR1GE 1410 bp mRNA linear PLN 15-NOV-1996
DEFINITION A.thaliana mRNA for peroxidase, prxr1.
ACCESSION   X98313
VERSION     X98313.1 GI:1402903
KEYWORDS    peroxidase; prxr1 gene.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE   1
AUTHORS     Capelli,N., Tognolli,M., Flach,J., Overney,S., Penel,C., Greppin,H.
              and Simon,P.
TITLE       Eleven cDNA clones from Arabidopsis thaliana encoding
              isoperoxidases (Accession Nos. X98313, X98314, X98315,
              X98317, X98318, X98319, X98320, X98321, X98322, and X98323)
JOURNAL     Plant Physiol. 112, 446-446 (1996)
REFERENCE   2 (bases 1 to 1410)
AUTHORS     Simon,P.
TITLE       Direct Submission
JOURNAL     Submitted (05-JUN-1996) P. Simon, Laboratory of Plant Biochemistry
              and Physiology, University of Geneva, Place de l'Universite 3,
              CH-1211 Geneva 4, SWITZERLAND
COMMENT     Ref [1]: Plant Gene Register PCR96-066 (1996).
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Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 1376 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 1403

RESULT 10
LOCUS       BX897675 68291 bp DNA linear PLN 16-DEC-2003
DEFINITION Neurospora crassa DNA linkage group IV BAC clone B2E7.
ACCESSION   BX897675
VERSION     BX897675.1 GI:39979158
KEYWORDS
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE   1
AUTHORS     Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Partmann,B.,
              Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.
JOURNAL     Unpublished
TITLE       (bases 1 to 68291)
JOURNAL     German Neurospora genome project.
AUTHORS     Direct Submission
TITLE       Submitted (16-DEC-2003) MIPS, Institut fuer Bioinformatik,
              GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
              Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
              G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
              of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
              E-mail: ulrich-schulte@uni-duesseldorf.de
JOURNAL     BAC clone 2E7 (strain OR74A) is available at the Fungal Genetic
              Stock Center, http://www.fgsc.net
AUTHORS     Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
              http://www.mwgna.com
JOURNAL     Information on performance of analysis and a more detailed
              annotation of this entry and other sequences can be viewed at:
              http://mips.gsf.de/proj/neurospora.
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  Location/Qualifiers

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Query Match          2.9%; Score 28; DB 8; Length 68291;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 41495 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 41468

RESULT 11
AC099530/c
LOCUS
DEFINITION Felis catus clone RP86-587N8, WORKING DRAFT SEQUENCE, 6 ordered
pieces.
AC099530
VERSION AC099530.2 GI:21070684
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 143793)
AUTHORS Akhtar, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee, L.S.-O., Legaspi, R., Maduro, O.L., Maduro, V.B.,
Margulies, E.H., Masello, C., Maskeri, B., Masrion, S.D.,
McCloskey, J.C., McDowell, J., Paquirigan, C., Pearson, R.,
Portnoy, J.E., Prasad, A., Schueler, M.G., Stancirpop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
REFERENCE 2 (bases 1 to 143793)
AUTHORS Green, E.D.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 143793)
AUTHORS Green, E.D.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2002) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
On May 22, 2002 this sequence version replaced gi:16930953.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142585 bases at least Q40
Consensus quality: 143084 bases at least Q30
Consensus quality: 143214 bases at least Q20
Insert size: 131000; agarose-fp
Insert size: 143293; sum-of-contigs
Quality coverage: 11.48X in Q20 bases; agarose-fp
Quality coverage: 10.50X in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 23243: contig of 23243 bp in length
* 23244 23343: gap of unknown length
* 23344 57299: contig of 33956 bp in length
* 57300 57399: gap of unknown length
* 57400 69014: contig of 11615 bp in length
* 69015 92456: gap of unknown length
* 92457 92557: contig of 23342 bp in length
* 92558 127282: gap of unknown length
* 127283 127383: contig of 34726 bp in length
* 127384 143793: contig of 16411 bp in length.
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JOURNAL

COMMENT

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Query Match      2.9%; Score 28; DB 2; Length 143793;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 955 CTTTTCATATAAAAAAAAAAAAAA 982
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Db 142830 CTTTTCATATAAAAAAAAAAAAAA 142803

RESULT 12
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DEFINITION Apis mellifera clone CH224-54J9, WORKING DRAFT SEQUENCE, 16
unordered pieces.

VERSION	AC141671.1	GI:29123855
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.	
SOURCE	Apis mellifera (honeybee)	
ORGANISM	Apis mellifera	

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.

REFERENCE
1 (bases 1 to 153829)

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Allbrooks, S.L., Anaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarta, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouhay, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burrett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, C., Denn, A.B., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hosi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Joilivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegod, H., Lozador, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, B., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwunigbo, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Schrager, S., Scott, G., Shen, H., Shoohtari, N., Sison, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabo, P., Tamerisa, K., Tamerisa, K., Tang, H., Tatey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleciyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE	Direct Submission	warnetclock,g:

FILE JOURNAL
Direct Submission
Unpublished

REFERENCE

AUTHORS
Worley, K.C.

TITLE	Direct Submission
1. TITLE	
2. AUTHOR(S)	
3. ADDRESS	
4. CITY	
5. STATE	
6. ZIP	
7. COUNTRY	
8. JOURNAL	
9. VOLUME	
10. NUMBER	
11. YEAR	
12. PAGES	
13. ABSTRACT	
14. KEYWORDS	
15. COMMENTS	

```
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ORIGIN

FEATURES	SOURCE
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/db_xref="taxon:7460"
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Query Match 2.9%; Score 28; DB 2; Length 153829;

Best Local Similarity 100.0%; Pred. No. 0.00065;

Matches	28	Conservative	0	Mismatches	0	Indels	0	Gaps	0
---------	----	--------------	---	------------	---	--------	---	------	---

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 955 CTTTGTGATATAAAAAAAAAAAAAAAAAA 982
 Db 71677 CTTTGTGATATAAAAAAAAAAAAAAAAAA 71650

RESULT 14
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 LOCUS
 DEFINITION Rattus norvegicus clone CH230-147P15, WORKING DRAFT SEQUENCE.
 ACCESSION AC103052
 VERSION AC103052.5 GI:30580047
 KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 217691)
 Murny,D,Marie., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alibrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,W., Baca,E., Baden,H.,
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 Mayhew,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
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 Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
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 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstock,G. and Gibbs,R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 217691)
 Worley,K.C.

TITLE Direct Submission
 JOURNAL Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 217691)
 AUTHORS Rat Genome Sequencing Consortium.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On May 13, 2003 this sequence version replaced gi:23614691.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GICH
 Center clone name: CH230-147P15
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 212164 bases at least Q40
 Consensus quality: 213776 bases at least Q30
 Consensus quality: 215303 bases at least Q20
 Estimated insert size: 223883; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 1 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces
 is believed to be correct as given, however the sizes
 of the gaps between them are based on estimates that have
 been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 217691: contig of 217691 bp in length.
 ----- Location/Qualifiers
 1. .217691
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 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-147P15"
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 /note="wgs_contig"

 Query Match 2.9%; Score 28; DB 2; Length 217691;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 955 CTTTGTGATATAAAAAAAAAAAAAAAAAA 982
 Db 13219 CTTTGTGATATAAAAAAAAAAAAAAAAAA 13192
 RESULT 15
 AC095577
 LOCUS AC095577 262093 bp DNA linear HTG 09-MAY-2003

DEFINITION Rattus norvegicus clone CH230-8G24, WORKING DRAFT SEQUENCE.
AC095577 GI:30467287
AC095577.6 GI:30467287
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 262093)
REFERENCE Murry,D,Marie., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Fligg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gregoire,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hayes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.J., Hodgson,A., Hogue,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangun,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhinney,S., McLeod,P.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwakenah,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Polinder,A., Popovic,D., Primus,E., Fu,L.-L., Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,E., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartbeyn,A., Sisson,I., Sitter,C.D., Smales,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmami,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhao,S., Zoon,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 262093)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 262093)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT
On May 9, 2003 this sequence version replaced gi:24940806.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCSX
Center Clone name: CH230-8G24
----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 239870 bases at least Q40
Consensus quality: 242191 bases at least Q30
Consensus quality: 243343 bases at least Q20
Estimated insert size: 257153; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 262093: contig of 262093 bp in length.

FEATURES
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1. 262093
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misc_feature
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Query Match 2.9% Score 28; DB 2; Length 262093;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982
DB 42589 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 42616
Search completed: September 26, 2004, 01:08:38
Job time : 4212.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 15:45:02 ; Search time 3100.47 Seconds
(without alignments)
9458.147 Million cell updates/sec

Title: US-10-069-527-3
Perfect score: 982
Sequence: 1-atggcgcggggaattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estlin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
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- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363.4	37.0	715	12	BI978526
2	354.2	36.1	624	12	BI977629
3	328	33.4	694	14	CB921382
4	307.8	31.3	502	13	BQ106725

5	307.8	31.3	503	13	BQ104750
6	306.4	31.2	710	13	BQ104750
7	299.2	30.5	497	13	BQ104187
8	295.2	30.1	639	13	BQ104187
9	293.8	29.9	605	13	BQ104187
10	293	29.8	762	14	CB9771393
11	288.2	29.3	692	14	CB972246
12	285	29.0	652	12	BI924444
13	284.6	29.0	698	10	AW737915
14	282	28.7	697	9	AJ568191
15	281.2	28.6	722	9	AJ568191
16	280.4	28.6	757	9	AJ568207
17	276.2	28.1	800	9	AJ568199
18	275	28.0	581	13	BQ104187
19	271.8	27.7	508	13	BQ104187
20	271.4	27.6	426	13	BQ106160
21	258	26.3	588	13	BQ106160
22	257.4	26.2	439	12	BI978252
23	255.2	26.0	727	14	CA990294
24	251.6	25.6	388	13	BQ104606
25	250.2	25.5	555	12	BI924402
26	244.8	24.9	642	14	CB087977
27	243	24.7	714	12	BI929568
28	240	24.4	573	12	BI929568
29	240	24.4	575	12	BI929568
30	236.8	24.1	590	10	AW624717
31	236.8	24.1	808	14	CB347452
32	235.8	24.0	605	12	BI928804
33	234.2	23.8	618	9	AI485411
34	234.2	23.8	670	9	AI484883
35	232	23.6	623	10	AW944760
36	230.2	23.4	576	12	BI929538
37	228.8	23.3	633	14	CB078399
38	228	23.2	582	9	AU089543
39	226.6	23.1	571	14	CB076679
40	225.8	23.0	585	14	CB626851
41	225.4	23.0	466	14	CB078943
42	224.8	22.9	471	14	CB079020
43	224	22.8	524	10	AW221174
44	223.8	22.8	541	12	BQ565775
45	223	22.7	520	9	AI483797

ALIGNMENTS

RESULT 1	BI978526	715 bp	mRNA	linear	EST 29-OCT-2002
LOCUS	u03	Old Blush petal	SMART library	Rosa chinensis	cdNA 5' similar
DEFINITION	to AP3 homologue (TW6), mRNA sequence.				
ACCESSION	BI978526				
VERSION	BI978526.1	GI:24420321			
KEYWORDS	EST.				
SOURCE	Rosa chinensis				
ORGANISM	Rosa chinensis				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.				
AUTHORS	Chaneliere, S., Riviere, S., Scalliet, G., Szecsi, J., Jullien, F., Dolle, C., Vergne, P., Dumas, C., Bendahmane, M., Huguency, P. and Cock, J.M.				
TITLE	Analysis of gene expression in rose petals using expressed sequence tags				
JOURNAL	FEBS Lett. 515 (1-3), 35-38 (2002)				
MEDLINE	21940574				
PUBMED	11943190				
COMMENT	Contact: Cock JM RDP (UMR5667 INRA/CNRS/ENSL/UCBL) Ecole Normale Supérieure de Lyon 46, Allée d'Italie, 69644 LYON Cedex 07, France Tel: 33472728611				

Fax: 33472728600

Email: Mark.Cock@ens-lyon.fr

PCR Primers

FORWARD: CTGCGAAGCGCGCCATTGTGTGGT

BACKWARD: ATACGACTCACTATAGGGCAATTGGCC.

FEATURES

Location/Qualifiers

1..715

/organism="Rosa chinensis"

/mol_type="mRNA"

/strain="Botanical garden, Lyon"

/cultivar="Old Blush"

/db_xref="taxon:74649"

/sex="Hermaphrodite"

/dev_stage="Mixed (young bud, open bud, mature flower, senescing flower)"

/lab_host="Escherichia coli"

/clone_lib="Old Blush petal SMART library"

/note="Organ: Petal; Vector: pTriplex2; Site_1: Sfil;

Site_2: Sfil"

ORIGIN

Query Match 37.0%; Score 363.4; DB 12; Length 715;

Best Local Similarity 76.0%; Pred. No. 7.5e-55;

Matches 489; Conservative 0; Mismatches 146; Indels 8; Gaps 3;

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QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCAGACCAACAGCGAGGTGACC 60
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DB 61 ATGGTCTGTGGAGATTGATGATCAAGCTGATCGAGAACAGACGACAGCGAGGTGACC 120
   |||||
QY 61 TACTCCAAAGAGAAATGGATCTTCAAGAGGCTCAGAGGTCAACGTTCTCTGTGAT 120
   |||||
DB 121 TATTGGAAGCGAAGATGGGATCTTCAAGAGGCTCAGAGGTCAACGTTCTGTGAC 180
   |||||
QY 121 GCCAAGTCTCCCTCATTTGCTCTCCACACATTAATAATGACGAGTATATCAGCCCT 180
   |||||
DB 181 GTCAGTCTCCCTCATTTGCTCTCCACACATTAATAATGACGAGTATATGACCCA 240
   |||||
QY 181 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATG 240
   |||||
DB 241 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATG 300
   |||||
QY 241 AGCACACAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
   |||||
DB 301 AGCTCACACTACGAGGCAATGAAAGAACTTGTGAAACTGAAAGAGGTTAACAATA 360
   |||||
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTCAGAG 360
   |||||
DB 361 CTGAGGAGAGATCAGGACAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTCAG 420
   |||||
QY 361 CTGGTCTCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
   |||||
DB 421 CTGCAAGATCTGGAGAAACGATGATGATGATGATGATGATGATGATGATGATGAT 480
   |||||
QY 421 CATGTGATCAAACTCAGACGAGAGACACCAAGAGAGGTTAAGAACTTGGAGCAAG- 479
   |||||
DB 481 CAGTGCTCAGACTCAGCAGAGACTTACCGAAGAAAGGTGAGAACTTGGAGGAGA 540
   |||||
QY 480 AAGAGGAAACATGCTGATGGCTATTTTTCACGAGGAGAGCGCGGCGAGGATCCAC 539
   |||||
DB 541 AACAGTAATTTTAAATGATGGCTATGAGGCTC-----CAGGTAATGAGGATCC 594
   |||||
QY 540 TGGTTATGAGCAATGAGGAGACTTACGAATCTGCATTTGATTTGATTTGAGGCGGA 599
   |||||
DB 595 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 654
   |||||
QY 600 TAACTTTGATACATTTCCACCTCCACCCCTAACCTCCACAC 642
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DB 655 -AACTTTGATTTTTCATTCCTCCGCTTCCACACACCAAC 696
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RESULT 2

BI977629

LOCUS

624 bp

mRNA

linear

EST 29-OCT-2002

DEFINITION

jd10 Old Blush petal SMART library Rosa chinensis cDNA 5' similar

to APETALA3 (BnAP3), mRNA sequence.

ACCESSION BI977629

VERSION BI977629.1

KEYWORDS GI:24419435

SOURCE EST.

ORGANISM Rosa chinensis

Rosa chinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

1 (bases 1 to 624)

Channeliere, S., Riviere, S., Scalliet, G., Szecsi, J., Jullien, F.,

Dolle, C., Vergne, P., Dumas, C., Bendahmane, M., Huguency, P. and

Cock, J.M.

Analysis of gene expression in rose petals using expressed sequence

tags

JOURNAL FEBS Lett. 515 (1-3), 35-38 (2002)

MEDLINE 21940574

PUBMED 11943190

COMMENT

Contact: Cock JM

RDP (UMR5667 INRA/CNRS/ENSL/UCBL)

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46, Allée d'Italie, 69364 LYON Cedex 07, France

Tel: 33472728611

Fax: 33472728600

Email: Mark.Cock@ens-lyon.fr

PCR Primers

FORWARD: CTGCGAAGCGCGCCATTGTGTGGT

BACKWARD: ATACGACTCACTATAGGGCAATTGGCC.

Location/Qualifiers

1..624

/organism="Rosa chinensis"

/mol_type="mRNA"

/strain="Botanical garden, Lyon"

/cultivar="Old Blush"

/db_xref="taxon:74649"

/sex="Hermaphrodite"

/dev_stage="Mixed (young bud, open bud, mature flower, senescing flower)"

/lab_host="Escherichia coli"

/clone_lib="Old Blush petal SMART library"

/note="Organ: Petal; Vector: pTriplex2; Site_1: Sfil;

Site_2: Sfil"

ORIGIN

Query Match 36.1%; Score 354.2; DB 12; Length 624;

Best Local Similarity 77.5%; Pred. No. 3.4e-53;

Matches 444; Conservative 0; Mismatches 123; Indels 6; Gaps 1;

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QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCAGACCAACAGCGAGGTGACC 60
   |||||
DB 58 ATGGTCTGTGGAGATTGATGATCAAGCTGATCGAGAACAGACGACAGCGAGGTGACC 117
   |||||
QY 61 TACTCCAAAGAGAAATGGATCTTCAAGAGGCTCAGAGGTCAACGTTCTCTGTGAT 120
   |||||
DB 118 TATTGGAAGCGAAGATGGGATCTTCAAGAGGCTCAGAGGTCAACGTTCTGTGAC 177
   |||||
QY 121 GCCAAGTCTCCCTCATTTGCTCTCCACACATTAATAATGACGAGTATATCAGCCCT 180
   |||||
DB 178 GCTCAGTCTCCCTCATTTGCTCTCCACACATTAATAATGACGAGTATATAGCCCA 237
   |||||
QY 181 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATG 240
   |||||
DB 238 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATG 297
   |||||
QY 241 AGCACACAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
   |||||
DB 298 AGCTCACACTACGAGGCAATGAAAGAACTTGTGAAACTGAAAGAGGTTAACAATA 357
   |||||
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTCAGAG 360
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DB 358 CTGAGGAGGAGATCAGGACAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTCAG 417
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/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc1070.e"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/note="vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      31.3%; Score 307.8; DB 13; Length 502;
Best Local Similarity 79.8%; Pred. No. 6.5e-45;
Matches 363; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAGATTGAATCAAGCTGATCGAAACAGACCAACAGGAGTCAAGGAGTGACC 60
Db 48 ATGGTCTGTGGAGATTGAGATCAAGCTGATCGAAACAGACCAACAGGAGTCAAGGAGTGACC 107

QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAAGGAGTCAAGGAGTGAT 120
Db 108 TATTCGAAGCGACGAATGGGATCTTCAAGAGGCTCAGGAGTCAAGGAGTCAAGGAGTGAT 167

QY 121 GCCAGGTCTCCCTCATATGCTCTCCACACTAATAAATGACAGAGTATATCAGCCCT 180
Db 168 GCTCAGGTCTCCCTCATATGCTCTCCACACTAATAAATGACAGAGTATATCAGCCCT 227

QY 181 ACCACTACGACCAAGAGTATGATGATCAATCAAGAAACTATGGGATCGATCTGTGG 240
Db 228 ACCACTACGACCAAGAGTATGATGATCAATCAAGAAACTATGGGATCGATCTGTGG 287

QY 241 AGGACACAGAGAGTGCATGAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAG 300
Db 288 AGCTCACACTACGAGGCAATGAAGAGAACTTTGGAAACTGAAAGAGGTTAAACAATAG 347

QY 301 CTGAGGAGAGATCAGGAGAGTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAG 360
Db 348 CTGAGGAGGACATCAGGCAAGGCTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAG 407

QY 361 CTGCGTTCTTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 408 CTGCAAGATCTGGAGGAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 467

QY 421 CATGTGATCAAACTCAGCGAGACCAACCAAGAA 455
Db 468 CACGTGCTCAAGACTCAAGCAGAGACTACCAGGAA 502

RESULT 5
BQ104750 503 bp mRNA linear EST 16-APR-2002
LOCUS fc1137.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
DEFINITION Rosa hybrid cultivar cDNA clone fc1137.e 5', mRNA sequence.
ACCESSION BQ104750
VERSION BQ104750.1 GI:20154412
KEYWORDS EST.
SOURCE Rosa hybrid cultivar
ORGANISM Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 503)
AUTHORS Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,
Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
Adam,Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and
Weiss,D.
TITLE Rose Scent: Genomics Approach to Discovering Novel Floral
Fragrance-Related Genes
JOURNAL Plant Cell 14 (10), 2325-2338 (2002)
COMMENT Contact: Naama Menda
Petat Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel

Tel: 972 8 9489 683
Fax: 972 8 9468 265
Email: shaham@agri.huji.ac.il
Seq primer: T3 forward.
Location/Qualifiers
source
1..503
/organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc1137.e"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/note="vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      31.3%; Score 307.8; DB 13; Length 503;
Best Local Similarity 79.8%; Pred. No. 6.5e-45;
Matches 363; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAGATTGAATCAAGCTGATCGAAACAGACCAACAGGAGTCAAGGAGTGACC 60
Db 48 ATGGTCTGTGGAGATTGAGATCAAGCTGATCGAAACAGACCAACAGGAGTCAAGGAGTGACC 107

QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAAGGAGTCAAGGAGTGAT 120
Db 108 TATTCGAAGCGACGAATGGGATCTTCAAGAGGCTCAGGAGTCAAGGAGTCAAGGAGTGAT 167

QY 121 GCCAGGTCTCCCTCATATGCTCTCCACACTAATAAATGACAGAGTATATCAGCCCT 180
Db 168 GCTCAGGTCTCCCTCATATGCTCTCCACACTAATAAATGACAGAGTATATCAGCCCT 227

QY 181 ACCACTACGACCAAGAGTATGATGATCAATCAAGAAACTATGGGATCGATCTGTGG 240
Db 228 ACCACTACGACCAAGAGTATGATGATCAATCAAGAAACTATGGGATCGATCTGTGG 287

QY 241 AGGACACAGAGAGTGCATGAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAG 300
Db 288 AGCTCACACTACGAGGCAATGAAGAGAACTTTGGAAACTGAAAGAGGTTAAACAATAG 347

QY 301 CTGAGGAGAGATCAGGAGAGTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAG 360
Db 348 CTGAGGAGGACATCAGGCAAGGCTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAG 407

QY 361 CTGCGTTCTTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 408 CTGCAAGATCTGGAGGAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 467

QY 421 CATGTGATCAAACTCAGCGAGACCAACCAAGAA 455
Db 468 CACGTGCTCAAGACTCAAGCAGAGACTACCAGGAA 502

RESULT 6
BQ875031 710 bp mRNA linear EST 16-OCT-2002
LOCUS V001F01 Populus flower cDNA library Populus balsamifera subsp.
DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION BQ875031
VERSION BQ875031.1 GI:24066555
KEYWORDS EST.
SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 710)
AUTHORS Unneberg,P., Bhale Rao,R.R., Jansson,S. and Sterky,F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
JOURNAL Unpublished (2002)

```

COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source
1. 710
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="rRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"

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Query Match 31.2%; Score 306.4; DB 13; Length 710;
Best Local Similarity 70.1%; Pred. No. 1e-44;
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACCGACCAACAGCGAGGTGACC 60
DB 85 ATGGGTCTGTGAAAGATTGAATCAAGAGATCGAAACCCCAACACAGCGAAGTCACC 144
QY 61 TACTCCAGAGAAAGATGGATCTTCAAGAGGCTCAGAGGCTCAGCGTTCTCTGTGAT 120
DB 145 TACTCGAAGAGAAATGGATGTTTCAAGAAACCCCAAGAACTCATGTACTTTGTGAT 204
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTAGTATCAGCGCT 180
DB 205 GCTAAGGTCTCTTTATCATGTTCTCCAACTAATAAATGACGAGTAGTATCAGCGCT 264
QY 181 ACCACTAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 265 TCCACATCGCAAAAGAGATCTACGATCAATATCAGAAACGCTTTAGGCATAGATCTGTG 324
QY 241 AGGACACACAGGAGTGCATGAAGACACCTTTGGGAAGTTGAAGAGATCAACAATAAG 300
DB 325 GGCACTCAATACGAGAAATGCAAGAGACCTTGGAGAGCTGAATGATATCAATCAATAG 384
QY 301 CTGAGGAGAGATGACGAGAGGTTGGGCAATGATCTAATGCGCTTGTGACGAG 360
DB 385 CTGAGACAAAGAAATCAGGAGAGGAGAGAGGCGCTGAATGATCTGAGCAATGATCAT 444
QY 361 CTGCGTTCTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 445 CTGCGCGCTCTTGACGACATATGATGATGATGATGATGATGATGATGATGATGATGATG 504
QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTGAAGACTTTGGAGCAAGA 480
DB 505 CATGTGATCAAAACACAAACAGAAACCTACAGGAAGAGGTGAAGATTTAGAGGAGAGA 564
QY 481 AGAGGAACATGTCGATGCTATTTTACGAGGAGACGCGCGGAGGATCCACAGTAT 540
DB 565 CATGGAACCT-----CTTGATGGAATATGAAGCAAACTTAGAGGATCGACAGTAT 615
QY 541 GGTATGAGGACATAGGAGAGTACGAAATCTGCACTTGCATTTGTCATTTGTCATTTGTCAT 600
DB 616 GGTATTAGGCAAT-----GAAGCTGCTGTGCACTTGCATTTGTCATTTGTCATTTGTC 663
QY 601 AACTGTACACTTCCACCTCCACCCCTTAACCTCCACCAC 642
DB 664 AACCTCTATGCTCCGCTGCTGATCAGGGGACACACCACC 705

RESULT 7
BQ104187
LOCUS 497 bp mRNA linear EST 16-APR-2002
DEFINITION fc2185.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
Rosa hybrid cultivar cDNA clone fc2185.e 5', mRNA sequence.
ACCESSION BQ104187

VERSION BQ104187.1 GI:20153849
KEYWORDS EST.
SOURCE Rosa hybrid cultivar
ORGANISM Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 497)
AUTHORS Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M.,
Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J.,
Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and
Weiss, D.
TITLE Rose Scent: Genomics Approach to Discovering Novel Floral
Fragrance-Related Genes
JOURNAL Plant Cell 14 (10), 2325-2338 (2002)
COMMENT Contact: Naama Menda
Petal Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel
Tel: 972 8 9489 683
Fax: 972 8 9468 265
Email: shaham@agri.huji.ac.il
Seq primer: T3 forward.
Location/Qualifiers
1. 497
/organism="Rosa hybrid cultivar"
/mol_type="rRNA"
/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc2185.e"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 30.5%; Score 299.2; DB 13; Length 497;
Best Local Similarity 79.2%; Pred. No. 2.2e-43;
Matches 355; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACCGACCAACAGCGAGGTGACC 60
DB 50 ATGGGTCTGTGGAAGATTGAGATCAAGCTGATCGAGAACCAAGACGACGAGGTGACC 109
QY 61 TACTCCAGAGAAATGGATCTTCAAGAGGCTCAGAGGCTCAGCGTTCTCTGTGAT 120
DB 110 TATTGAAAGCAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCAGCGTTCTGTGTGAC 169
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTAGTATCAGCGCT 180
DB 170 GCTCAGGTTTCTCATCATCATGCTCCTCCACTGACAAATCCACGAGTATATTAGCCCA 229
QY 181 ACCACTAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 230 ACCACTAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 289
QY 241 AGGACACACAGGAGTGCATGAAGACACCTTTGCGAAGTTGAAAGAGATCAACAATAAG 300
DB 290 AGCTCACACTACAGGCAATGAAAGAGACTTGTGGAACCTGAAGAGGTTTAACATAAG 349
QY 301 CTGAGGAGAGATCAGGAGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAG 360
DB 350 CTGAGGAGGACATCAGGCAAGGCTGGGGCATGATCTTAATGGTCTGAGCTATCTGAG 409
QY 361 CTGGCTTCTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 410 CTGCAAGATCTGGAGGAAACGATGATGATGATGATGATGATGATGATGATGATGATG 469
QY 421 CATGTGATCAAACTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 448
DB 470 CACGTGCTCAAGACTCAAGCAGAGAGACTA 497

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RESULT 8
BU879075          639 bp      mRNA      linear      EST 16-OCT-2002
DEFINITION
V055E10 Populus flower cDNA library Populus balsamifera subsp.
trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
BU879075          1 GI:24070599
VERSION
KEYWORDS
SOURCE
ORGANISM
Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 639)
REFERENCE
Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,P.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
JOURNAL
COMMENT
Contact: BHALERAO RUPALI R.
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
FEATURES
source
1..639
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
ORIGIN
Query Match          30.1%; Score 295.2; DB 13; Length 639;
Best Local Similarity 71.0%; Pred. No. 1e-42;
Matches 409; Conservative 0; Mismatches 158; Indels 9; Gaps 1;

Qy 1 ATGCGCGCGGGAAGATTGAAATCAAGCTCATCGAAACCCAGACCACAGCGAGGTGACC 60
Db 71 ATGGTCTGTGAAGATTGAAATCAAGAGATCGAAACCCCAACACAGCGCAAGTCACC 130

Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGGCTACCGTTCTCTGTGAT 120
Db 131 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 190

Qy 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACACTAAATAAATGACAGGATATATCAGCCCT 180
Db 191 GCTAAGTCTCTTATCATGTTCTCCACACCTAACCAACTCAATGAGTACATTAGSCCCC 250

Qy 181 ACCACTACGACCAAGAGATATGATATGATCTATCAGAAAACTATGGGGATTCGATCTGTGG 240
Db 251 TCCACATCGCAAGAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 310

Qy 241 AGGCACACAGAGGATCGATGAAAGACACCTTGTGGAGTTGAAAGAGATCAACATATAG 300
Db 311 GGCACTCAATACGAGAAAATGCAAGAGCACTTGAAGAGCTGAATGATATCAATCATATAG 370

Qy 301 CTGAGGAGAGAGATCAGGCGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360
Db 371 CTGAGACAAGAAATCAGGCGAGGAGAGAGAGGCGCTGAATGATCTGAGCAATTGATCAT 430

Qy 361 CTGGCTTCTTTCAGATGAGATGCACTTCTTCGATGCCATAGCTCAAGAGGAGTAC 420
Db 431 CTGCGCGGTCTTTCAGCAACATATGACTGAAGACCTTGAATGGTGTGGTGGCAGGAAGTAC 490

Qy 421 CATGTGATCAAAATCTAGACGGAGACCAACCAAGAAAGGTTAAGAACTTTGGAGCAAGA 480
Db 491 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAATTTAGAGGAGAGA 550

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Qy 481 AGAGAAACATGCTGCATGCTATTTTTCACCCAGGAAGCAGCGCGGAGGATCCACAGTAT 540
Db 551 CATGAAACCT-----CTTGATGAATATGAAGCAAACTAGAGGATCGACAGTAT 601

Qy 541 GGTATGAGGCAATGAGGAGACTAGATCTGCA 576
Db 602 GGTATGAGGCAATGAGGCTGCTGTTCCACTTGA 637

RESULT 9
BU877396          605 bp      mRNA      linear      EST 16-OCT-2002
LOCUS
V033E07 Populus flower cDNA library Populus balsamifera subsp.
trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
BU877396          1 GI:24068920
VERSION
KEYWORDS
SOURCE
ORGANISM
Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 605)
REFERENCE
Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,P.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
JOURNAL
COMMENT
Contact: BHALERAO RUPALI R.
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
FEATURES
source
1..605
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
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Query Match          29.9%; Score 293.8; DB 13; Length 605;
Best Local Similarity 70.1%; Pred. No. 1.9e-42;
Matches 413; Conservative 0; Mismatches 167; Indels 9; Gaps 1;

Qy 2 TGGCGCGCGGGAAGATTGAAATCAAGCTCATCGAAACCCAGACCACAGCGAGGTGACCT 61
Db 16 TGGTCTGTGGAAGATTGAAATCAAGAGATCGAAACCCCAACACAGGCAAGTCACCT 75

Qy 62 ACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCAGGCTCAGCTTCTCTGTGATG 121
Db 76 ACTCGAAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTATCTTTGTGATG 135

Qy 122 CCAAGTCTCCCTCATTTATGCTCTCCAACTATAATAAATGCAGAGTATATCAGCCCTA 181
Db 136 CTAGGTCTCTTATCATGTTCTCCAACTATAAATACTAATGATGATACATTAGCCCT 195

Qy 182 CCATTCAGCCCAAGAGTATGATGATGATCTATCAGAAAACTATGGGATGATCTGTGGA 241
Db 196 CCATTCAGCAAGAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 255

Qy 242 GGACACACAGAGGTCGATGAAAGACACCTTGTGCAAGTTGAAAGAGATCAACAATAAGC 301
Db 256 GCATCAATACGAGAAATGCAAGAGCACTTGAGAGAGCTGAATGATATCAATCATATAGC 315

Qy 302 TGAGGAGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAGC 361
Db 316 TGAGACAAGAAATCAGGCGAGAGAGAGAGGAGGCGCTGAATGATCTGAGCATTCATC 375

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362 TGGCTTCTTGGAGATGAGATGCTTCTCTTGGATGCCATACGTCAAGGAAGTACC 421
 Db TGGCGGCTTGGAGCAACATATGACTGAAGCTTGAATGGTGTGGTGGCAGGAATACC 435
 Qy ATGTGATCAAACTCAGAGGAGACCCACCAAGAGAGAGGTTAAGAACTTGGAGCAAGAA 481
 Db ATGTGATCAAAACACAAACCAACCTACAGGAAGAGGTTAAGAACTTGGAGGAGAC 495
 Qy GAGGAAACATGCTGATGGCTATTATTGACAGGAGAGCGCGGAGGATCCACAGTATG 541
 Db ATGGAACCTTTGACGGAATAT-----GAGCAAACTAGAGATGACAGTATG 546
 Qy GTTATGAGGACATGAGGAGACTACGAATCTGCACCTTGCAATGTCATAA 590
 Db GTTATGAGCAATTGAGCTGCTGTTGCACTTGCAATGGGCTTCCAA 595

RESULT 10
 CB971393 762 bp mRNA linear EST 30-APR-2003
 LOCUS CAB10005_Iia_Fa_B07 Cabernet Sauvignon Flower Pre-bloom - CAB1
 DEFINITION Vitis vinifera cDNA clone CAB10005_Iia_Fa_B07 5', mRNA sequence.
 ACCESSION CB971393
 VERSION EST.
 KEYWORDS CB971393.1 GI:30254946
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 762)
 Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and
 Cook, D.
 Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
 berries at various developmental stages
 Unpublished (2003)
 Contact: Douglas Cook, PhD
 CAES Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcook@ucdavis.edu
 Seq primer: ACGGTACCGACATATGCC.

FEATURES

1...762
 Location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB10005_Iia_Fa_B07"
 /sex="Hermaphrodite"
 /dev_stage="Pre-bloom"
 /lab_hosts="DHSalpha"
 /clone_libs="Cabernet Sauvignon Flower Pre-bloom - CAB1"
 /note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1:
 Sfil; Site_2: Sfil; CAB1 is a cDNA library of Vitis
 vinifera cv. 'Cabernet Sauvignon'. Clone 8 flowers. Samples
 were collected approximately eleven days before onset of
 bloom (clusters at this stage were fully developed and
 flowers with calyxtras or caps still attached. Sampled
 vines were located at the University of California, Davis,
 Experimental Vineyard. cDNAs were made by oligo-dT priming
 and directionally cloned. 5' and 3' adaptors were used in
 cloning as follows:
 5'-AAGAGTGTATCAACGAGAGTGGCATTCAGCGCGG-3' and
 5'-ATTCTAGGCGCGGCGGACATG-dt(30)NN-3'. Library was
 constructed using the Clontech Creator SMART kit and
 size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 29.8%; Score 293; DB 14; Length 762;

Best Local Similarity 69.8%; Pred. No. 2.4e-42; Mismatches 414; Conservative 0; Mismatches 170; Indels 9; Gaps 1;
 Qy 1 ATGGCGCGGGAAGATTCAAAATCAAGCTGATGCAAAACACAGCAACAGGAGGTGACC 60
 Db ATGGCTAGAGGAAGATTGAGATCAAGAGATAGAGAACTCGACGAACAGGAGGTACCC 69
 Qy TACTCTCAAGAGAGAAATGGGATCTTTCAAGAAGGCTCAGGAGCTCACCGTTCTGTGTAT 120
 Db TACTCTCAAGAGAGAAATGGTATCTTTCAAGAAGGCCAGTGAGCTCACTGTTCTTTGTAT 129
 Qy 121 GCGAAGTCTCCTCATNTATGCTCTCCACACTATAATAATGACGAGATATATCAGCCCT 180
 Db 130 GCTAAGGTTTCTATCATCATGCTCTCCAGTACTTGGAAAGCTCATGAATACATCAGCCCT 189
 Qy 181 ACCACTACGACCAAGAGATGATGATGACTACTATCAGAAAACCTATGGGATCGATCTGTGG 240
 Db 190 TCCACTACAACGAAACAAATATTTGATCAGTACCAGAACACTCTAGGAGTGGATCTATGG 249
 Qy 241 AGACACACAGAGAGTCGATGAAGACACCTTGTGGAGTCTTGAAGAGATCAACAATAAG 300
 Db 250 AGCTATCACTATGAGAGAATGCAAGAAAACCTGAAAGAACTGAAAGATGTGAACAAGAT 309
 Qy 301 CTGAGGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCTGAGCTTTGACGAG 360
 Db 310 CTCAGGAAGAGATTAGGCGAGAGTGGTGAACATTTGAGCGATTGAGCGTTGAGGAA 369
 Qy 361 CTGGCTTCTTTCAGCATGAGATGAGTCTTCTTGGATGCCATACGTCAAGGAGATGAC 420
 Db 370 CTGCGAGATCTTGAACACAGAGATGGAGATTTCTTTGAAGATGTTCTGATAGGAATGAC 429
 Qy 421 CATGTGATCAAACTCAGACGAGAGCCACCAAGAGAGGTTAAGAACTTTGAGGCAAGAA 480
 Db 430 CAGGTGATCAATAATCAGATTGAACCTTTCAAGAAAAGGTAAGGAATGTGGAACAATA 489
 Qy 481 AGAGGAAACATGCTGCATGGCTATTTTGACAGGAGACGCCGCGGAGGATCCACAGTAT 540
 Db 490 CACAAAAATCTCTACATGAATTT-----GATGCAAGGAGACAGATCAATACTAT 540
 Qy 541 GGTATGAGCAATGAGGAGACTACGAATCTGCATTCGATTGCAATGG 593
 Db 541 GGGCTAGTGACAATGGAGGGGATTACGAATCTGTTCTTGGATTCTCAATGG 593

RESULT 11

CB972246

LOCUS CB972246 692 bp mRNA linear EST 30-APR-2003
 DEFINITION CAB10006_Ia_Fa_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis
 vinifera cDNA clone CAB10006_Ia_Fa_D07 5', mRNA sequence.

ACCESSION

CB972246

VERSION

CB972246.1 GI:30256403

KEYWORDS

EST.

SOURCE

Vitis vinifera

ORGANISM

Vitis vinifera

REFERENCE

1 (bases 1 to 692)

AUTHORS

Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and
 Cook, D.

TITLE

Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
 berries at various developmental stages

JOURNAL

Unpublished (2003)

COMMENT

Contact: Douglas Cook, PhD
 CAES Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcook@ucdavis.edu
 Seq primer: ACGGTACCGACATATGCC.

FEATURES

Location/Qualifiers

1...692

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clones="CAB10006_Ia_Fa_D07"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DHSalpha"
/clone_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"
Sfil: Site_2: Sfil; CAB1 is a cDNA library of Vitis vinifera cv. Cabernet Sauvignon. Clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and vines with calypters or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGTGGCCATTACGGCCGG-3' and 5'-ATTAGAGCCGCGGCGGCATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 29.3%; Score 288.2; DB 14; Length 692;
Best Local Similarity 69.3%; Pred. No. 1.8e-41;
Matches 411; Conservative 0; Mismatches 173; Indels 9; Gaps 1;
QY 1 ATGCGCGCGGAGATTGAAATCAACTGATCGAAACACAGACACAGGAGGTGACC 60
DB 51 ATGCTAGAGGAAGATTGAGATCAAGAGATAGAGACTCGACGACAGGAGGTCA 110
QY 61 TACTCCAGAGAGAAGATTGGAATCTCAAGAGGCTCAGAGGTCAACCGTCTCTGTGAT 120
DB 111 TACTCCAGAGAGCAAGATTGATCTTCAAGAGGCCAGTCACTGCTCTCTGTGAT 170
QY 121 GCCAAGTCTCCCTCATTTATGCTCTCAACACATTAATAATGACGAGTATACGCCCT 180
DB 171 GCTAAGGTTTCTATCATGCTCTCCAGTACTGGAAGCTCCATGATACATCAACCC 230
QY 181 ACCACTACGACCAAGATGTATGATGACTATCAGAAAATATGGGGATCGATCTGTGG 240
DB 231 TCCACTACAGCAACAAATATTGATCAGTACCAAGCACTCTAGGAGTGGATCTATGG 290
QY 241 AGGACACAGGAGTGCATGAAGACACCTTGTGGAGTTGAAGAGATCAACATTAAG 300
DB 291 AGCTATCACTATGAGAAATGCAAGAAACCTGAAGAACTGAAGATGTGAACAAGAT 350
QY 301 CTGAGGAGAGATCAGCGAGAGTTGGGCGCATGATCTAAATGGCTTGAGCTTTCAGCG 360
DB 351 CTCAGGAAGGAGATTAGCGAGAGATGGTGAACATTTGAGCGATTGAGCGTTGAGAA 410
QY 361 CTGCGCTCTCTGAGATGAGATGCTCTCTTGTGATGCCATAGCTCAAGGAAGTAC 420
DB 411 CTGCGAGATCTTGAAACAGAGATGGAGAGTTCTTTGAAGATGGTTCGTGATAGGAAGTAC 470
QY 421 CATGTGATCAAACTCAGACGGAGACCAACCAAGAGAGTTGAAGTCTGAGCAAGAA 480
DB 471 CAGTGATCAATATCAGATTGAACCTTTCAGAAACCGTGAAGATGTGGAACAAATA 530
QY 481 AGAGAAACATGTGCGATGCTATTTTGAACAGGAAGACCGCGGAGGATCCACAGTAT 540
DB 531 CACAAAATCTCTACATGAATTT-----GATCAGGAGGACAGATCAATCTCTAT 581
QY 541 GGTATCAGGACATGAGGAGACTACGAATCTGCACTTCGATTTGTCATGTCATGG 593
DB 582 GGGCTAGTGACATGAGGGGATTACGAATCTGTTCTTGATTTCTCAATGG 634

RESULT 12
BI924444
LOCUS

DEFINITION EST544333 tomato flower, buds 0-3 mm Lycopersicon esculentum cDNA clone CTOA23G18 5' end, mRNA sequence.
ACCESSION BI924444
VERSION BI924444.1 GI:16227773
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE 1 (bases 1 to 652)
AUTHORS van der Hoeven,R.S., Bezzerides,J.L., Karanycheva,S.A., Tsai,J., Uterback,I., Van Aken,S., Roming,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
TITLE Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.
FEATURES
Location/Qualifiers
1..652
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clones="CTOA23G18"
/tissue_type="flower"
/dev_stage="0-3mm buds"
/clone_lib="tomato flower, buds 0-3 mm"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Query Match 29.0%; Score 285; DB 12; Length 652;
Best Local Similarity 67.4%; Pred. No. 6.7e-41;
Matches 421; Conservative 0; Mismatches 195; Indels 9; Gaps 1;
QY 2 TGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGCAACAGGAGGTGACCT 61
DB 1 TGGCGCGTGGAAAATTTGAGATCAAGAAATTTGAAAATCTGACAAACAGGCGAGTCT 60
QY 62 ACTCAAGAGAAAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGATG 121
DB 61 ACTCAAGAGAAAGAAACGGTATTTTCAAGAAAGCTAAGAACTTACTGTTCTTGTGACG 120
QY 122 CCAAGGTCCTCCCTCATTTATGCTCTCAACACTATAATAATGACGAGTATATCAGCCCTA 181
DB 121 CTAAGATCTCTCTCATCATGCTATCAAGCCACCAAGAAAGTATCATGAGTACCAAGCCAA 180
QY 182 CCATCTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
DB 181 ACATCTACGACCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 242 GGACACACGAGAGTTCGATGAAGACACCTTTGGAGTTGAAAGATCAACAAATAGC 301
DB 241 GCATTCATCTACGAGAAATGCAAGAAATCTGAAAGATTCAGAAAGATCAATTAACAGC 300
QY 302 TGAGGAGAGATCAGGACAGAGGTTGGCCATGATTAATGGCTCAGCTTTTCACGAGC 361
DB 301 TAAGAGAGATTAAGCGAGAGAAACAGGGGAACATGACGGGACTAAATTTGACGAGAC 360
QY 362 TGGCTTCTCTTACGATGAGATGAGTCTTCTTCTTGGATGCCATACGTCACAAAGGATACC 421
DB 361 TATGTCACCTTGCAGAGAAACATCACTGAATCTGTTGCTGAGATTCGTGAACGAAATACC 420

QY 422 ATGTGATCAAACTCAGACGGAGACCAACGAAGAAGGTTAAGAACTTGGAGCAAGAA 481
 Db 421 ACGTGATCAAGAAATCAAAACAGACACCTCGCAAGAAGAAGGCGAGAACTTGAAGAGCAAA 480
 QY 482 GAGGAACATGCTGCATGGCTATTTCACAGGAGAGCAGCGCGAGGATCCACAGTATG 541
 Db 481 ATGGAACCTTGATC-----TTGACTTGGAGCAAAATGTGAAGATCCAAAGTATG 531
 QY 542 GTTATGAGCAATGAGGAGACTACGAATCTGCATTTGCATTTGATTTCAAAATGGGCGGAATA 601
 Db 532 GTGTTGTGGAATAAGAGGGGCAATACCACCTGCTGTGGCAATTTGCCAATGGAGTACACA 591
 QY 602 ACTTGATACATTTCCACTCCACCA 626
 Db 592 ATCTTTATGCTTTTCGGCTACAACA 616

RESULT 13
 LOCUS AW737915 698 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST333342 tomato flower buds, anthesis, Cornell University
 Lycopersicon esculentum cDNA clone cTOD4L21 5', mRNA sequence.
 ACCESSION AW737915
 VERSION AW737915.1 GI:7646860
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum

REFERENCE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 698)
 van der Hoeven,R.S., Bezzerides,J.L., Matern,A.L., Holt,I.E.,
 Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Rinning,C.M.,
 Nieman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
 Tanksley,S.D.
 Generation of ESTs from tomato flower tissue, anthesis
 Unpublished (1999)
 CONTACT: CUGI
 CLEMSON UNIVERSITY
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
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 /organism="Lycopersicon esculentum"
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 /db_xref="taxon:4081"
 /clone="cTOD4L21"
 /tissue_type="flower"
 /dev stage="anthesis"
 /clone_lib="tomato flower buds, anthesis, Cornell
 University"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; supplier: Tanksley; Flower buds and flowers were
 taken from greenhouse plants (4-8 wks old, TA496). They
 were immediately frozen in liquid nitrogen and then
 size-separated while remaining frozen."

ORIGIN
 source
 Query Match 29.0%; Score 284.6; DB 10; Length 698;
 Best Local Similarity 66.7%; Pred. No. 7.6e-41;
 Matches 426; Conservative 0; Mismatches 204; Indels 9; Gaps 1;
 QY 2 TGGCGCGGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCAGGTGACCT 61
 Db 1 TGGCGCGTGGAAATTTGAGATCAAGAGATTGAATCTGCAACAGCAGGTCACTT 60
 QY 62 ACTCCAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGATG 121
 Db 61 ACTCCAAGAGAGAAACGGTATTTTCAAGAAAGCTAAGAACTTACTGTCTTTGTGACG 120

QY 122 CCAAGTCTCCCTCTATTATGCTCTCAACACTAATAAATGCACAGTATATCAACCCCTA 181
 Db 121 CTAAGATCTCTCTCTCATGCTATCAAGCACAGGAAGTATCATGAGTACACAGACCCCA 180
 QY 182 CCACTACGACCAAGAGTATGATGATCTATCAGAAACTATGGGATCGGATCTGTGGA 241
 Db 181 ACACCTACGACCAAAAGATGATGATCAGATCAGATGCGACTTGGAGTTGATATCTGGA 240
 QY 242 GGACACACAGGAGTGCATGAAAGACACCTTGTGAAAGTTGAAGAGATCAACAATAAGC 301
 Db 241 GCATTCACCTACGAGAAATGCAAGAAACTTGAAGAGATTGAAGAGATCAATAACAAGC 300
 QY 302 TGAGGAGAGAGATCAGGAGAGGTTGGCCATGATCTAAATGGCCCTGAGCTTTCAGGAGC 361
 Db 301 TAAGAAGAGAGATAAGGAGAGAACAGGGGAAGACATGAGCGGACTAAATTTGCGAGGAAC 360
 QY 362 TGGCTTCTCTGACGATGAGATGCACTCTTCTTGGATGCCATACGTCAAGAAAGTATCC 421
 Db 361 TATGTCACCTTGCAGGAGAACATCACTGAATCTGTTGCTGAGATTCGTGAACGAAAGTACC 420
 QY 422 ATGTGATCAAACTCAGACGGAGACCAACGAAGAAGTTAAGAACTTGGAGCAAGAA 481
 Db 421 ACGTGATCAAGAATCAACAGACACCTCGAAGAAGAGCGGAGAACTTAGAAGAGCAAA 480
 QY 482 GAGGAAACATGCTGCATGGCTATTTTGACCAAGAAAGCAGCGCGGAGATCCACAGTATG 541
 Db 481 ATGGAACCTTGATC-----TTGACTTGGAGCAAAATGTGAAGATCCAAAGTATG 531
 QY 542 GTTATGAGCAATGAGGAGACTACGAATCTGCACTTGCATTTGCAATGGGCGGAATA 601
 Db 532 GTGTTGTGGAATAAGAGGGGCAATACCACCTCTGCTGTGGCAATTTGCGAATGGAGTACACA 591
 QY 602 ACTTGATACATTTCCACCTCCACCCCTTAACCTCCACC 640
 Db 592 ATCTTTATGCTTTTCGCTACAAACCATTCGCCCAATC 630

RESULT 14
 LOCUS AJ568191 697 bp mRNA linear EST 28-JUL-2003
 DEFINITION AJ568191 Antirrhinum majus library (Stueber K) Antirrhinum majus
 cDNA clone zschol3a, mRNA sequence.
 ACCESSION AJ568191
 VERSION AJ568191.1 GI:33294080
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snapdragon)
 ORGANISM Antirrhinum majus

REFERENCE
 1 (bases 1 to 697)
 Stueber,K. and Schwarz-Sommer,Z.
 Antirrhinum majus EST collection (Stueber,K. and Schwarz-Sommer,Z.)
 Unpublished (2003)
 CONTACT: Stueber K
 Molecular Plant Genetics
 MPI fuer Zuechtungsforshung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
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ORIGIN
 source
 Query Match 28.7%; Score 282; DB 9; Length 697;
 Best Local Similarity 67.2%; Pred. No. 2.2e-40;
 Matches 418; Conservative 0; Mismatches 195; Indels 9; Gaps 1;

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QY 1 ATGGCGCGGGAGATTGAATCAAGCTGATCGAAAAACAGACCAACAGGCGAGGTGACC 60
Db 38 ATGGCTCGAGGAGAGATCCAGATTAAGAGATGAGAGACCAACCAACAGGCGAGGTGACC 97
QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGTCAACCGTTCTCTGTGAT 120
Db 98 TACTCCAGAGAGAAATGGTTGTTCAAGAGAGCACAGGCTCTCTGTCTCTGTGAT 157
QY 121 GCCAAGTCTCCCTCATTTGCTCTCAACACATTAATAATGACGAGTATATCAGCCCT 180
Db 158 GCTAAAGTTTCCATTATCATGATCTCCGTAATCAAGAGCTTCAAGAAATATATCAGCCCA 217
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240
Db 218 ACAAATCGCAAGACAGTTATTTCGATCAGTATCAGAAAGCCGTTGGAGTTGATCTATGG 277
QY 241 AGNACACAGGAGTGCATGAAGACACCTTTGTGGAAGTTGAAGAGATCAACAATAG 300
Db 278 AGCTCACACTATGAGAAATGCAAGAGACACTTGAAGAGCTGAATGAGGTCAACAGGAAT 337
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTMAATGGCCTGAGCTTTGACGAG 360
Db 338 CTGAGGAGGAGATCAGCAAGAGTGGGTGAGAGCTTGAACGATCTGGGCTACGACAA 397
QY 361 CTGGCTTCTCTGACGATGAGTGCAGTCTTCTGATGCCATACGTCAAAGGAAGTAC 420
Db 398 ATTGTGAATCTTATTGAAGACATGGATACTCTCAAGCTCATCTCGTGAAGAAAGTAC 457
QY 421 CATGTGATCAAACTCAGACGGAGACCAACCAAGAGAGTTAAGAACTTGGAGCAAGA 480
Db 458 AAGTCAATCAGTAACCAAGATCGACCCGACGAGAAAGTACAGGAATGTTGAAGAAATA 517
QY 481 AGAGAAACATGCTGCATGCTATTTTGACCAAGAGACGCGGAGGATCCACAGTAT 540
Db 518 CACAGAAACCTGGTGC-----TTGAATTTGATGCAAGGAGAGAGGATCCACACTTT 568
QY 541 GGTATGAGACATGAGGAGATCAGATCTGCATCTGCATTTGATGTCATGTCGAGGAGAT 600
Db 569 GGATTAGTATGATGAAGTGATTAATATCTGTCTCTGTTTCCCAATGAGGGGCT 628
QY 601 AACTTGTACACTTTCCACCTCC 622
Db 629 CGTATATCGCCTACGCTCC 650

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RESULT 15
AJ559554
LOCUS
DEFINITION
AJ559554 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018_1_10_k11, mRNA sequence.
ACCESSION
AJ559554
VERSION
AJ559554.1 GI:31662126
KEYWORDS
EST.
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Antirrhinaceae; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 722)
Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
CONTACT: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="whole plant"
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ORIGIN

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Query Match      28.6%; Score 281.2; DB 9; Length 722;
Best Local Similarity 65.6%; Pred. No. 3e-40;
Matches 450; Conservative 0; Mismatches 218; Indels 18; Gaps 2;

QY 1 ATGGCGCGGGAGATTGAATCAAGCTGATCGAAAAACAGACCAACAGGCGAGGTGACC 60
Db 24 ATGGCTCGAGGAGAGATCCAGATTAAGAGATGAGAGACCAACCAACAGGCGAGGTGACC 83
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAACCGTTCTCTGTGAT 120
Db 84 TACTCCAGAGAGAAATGGTTGTTCAAGAGAGCACAGGCTCTCTGTCTCTGTGAT 143
QY 121 GCCAAGTCTCCCTCATTTGCTCTCAACACATTAATAATGACGAGTATATCAGCCCT 180
Db 144 GCTAAAGTTTCCATTATCATGATCTCCAGTACTCAGAAAGCTTCAAGAAATATATCAGCCCA 203
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240
Db 204 ACAAATCGCAAGACAGTTATTTCGATCAGTATCAGAAAGCCGTTGGAGTTGATCTATGG 263
QY 241 AGNACACAGGAGTGCATGAAGACACCTTTGTGGAAGTTGAAGAGATCAACAATAG 300
Db 264 AGCTCACACTATGAGAAATGCAAGAGACACTTGAAGAGCTGAATGAGGTCAACAGGAAT 323
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTMAATGGCCTGAGCTTTGACGAG 360
Db 324 CTGAGGAGGAGATCAGCAAGAGTGGGTGAGAGCTTGAACGATCTGGGCTACGACAA 383
QY 361 CTGGCTTCTCTGACGATGAGTGCAGTCTTCTGATGCCATACGTCAAAGGAAGTAC 420
Db 384 ATTGTGAATCTTATTGAAGACATGGATACTCTCAAGCTCATCTCGTGAAGAAAGTAC 443
QY 421 CATGTGATCAAACTCAGACGGAGACCAACCAAGAGAGTTAAGAACTTGGAGCAAGA 480
Db 444 AAGTCAATCAGTAACCAAGATCGACCCGACGAGAAAGTACAGGAATGTTGAAGAAATA 503
QY 481 AGAGAAACATGCTGCATGCTATTTTGACCAAGAGACGCGGAGGATCCACAGTAT 540
Db 504 CACAGAAACCTGGTGC-----TTGAATTTGATGCAAGGAGAGAGGATCCACACTTT 554
QY 541 GGTATGAGACATGAGGAGATCAGATCTGCATCTGCATTTGATGTCATGTCGAGGAGAT 600
Db 555 GGATTAGTATGATGAAGTGATTAATATCTGTCTCTGTTTCCCAATGAGGGGCT 614
QY 601 AACTTGTACACTTTCCACCTCC-----CACACCCCTAACCTCCACGAGGAGGAGC 651
Db 615 CGTATAATCGCCCTACGCTCCCGAGCTAATCACCATCTCTCTTTCACAGCGGAGGGGC 674
QY 652 TCGTCTCGGCTCTCCATCTACTCTCT 677
Db 675 TCTGATCTCACCACCTTTTGTCTTCT 700

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Search completed: September 25, 2004, 22:02:28
 Job time : 3104.47 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 16:09:57 ; Search time 539.304 Seconds
(without alignments)
9222.595 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcgaggattga.....aaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306.4	31.2	681	15	US-10-104-580-3
2	306.4	31.2	946	15	US-10-104-580-2
3	257.8	26.3	1050	13	US-10-425-114-12758
4	252.4	25.7	1231	13	US-10-425-114-15025
5	250.8	25.5	1212	13	US-10-425-114-11957
6	246	25.1	1155	13	US-10-424-599-66649
7	240.2	24.5	1036	13	US-10-424-599-120794
8	238.4	24.3	644	17	US-10-021-323-8631
9	231.8	23.6	871	13	US-10-425-114-10670
10	228	23.2	498	12	US-09-732-627A-4479
11	217.4	22.1	681	16	US-10-260-238-5330
12	194.6	19.8	237	13	US-10-425-114-13190
13	192	19.6	2718	13	US-10-424-599-120795
14	191	19.5	407	12	US-09-922-293-3294

Sequence 14, Appl	15	186.4	19.0	425	12	US-09-922-293-14
Sequence 13, Appl	16	182	18.5	401	12	US-09-922-293-13
Sequence 16, Appl	17	181.6	18.5	432	12	US-09-922-293-16
Sequence 3447, Ap	18	176.8	18.0	365	12	US-09-922-293-3447
Sequence 3446, Ap	19	168.8	17.2	422	12	US-09-922-293-3446
Sequence 15, Appl	20	166.2	16.9	360	12	US-09-922-293-15
Sequence 8506, A	21	164.6	16.8	503	13	US-10-424-599-85506
Sequence 380, App	22	158.2	16.1	340	12	US-09-732-627A-380
Sequence 337, App	23	146.6	14.9	309	12	US-09-732-627A-337
Sequence 3442, Ap	24	146.4	14.9	253	12	US-09-922-293-3442
Sequence 3444, Ap	25	143.2	14.6	293	12	US-09-922-293-3444
Sequence 2121, Ap	26	139.4	14.2	951	17	US-10-767-795-2121
Sequence 14870, A	27	137.6	14.0	1007	13	US-10-425-114-14870
Sequence 6326, A	28	137.6	14.0	1021	13	US-10-424-599-6326
Sequence 4667, Ap	29	135.8	13.8	474	12	US-09-732-627A-4667
Sequence 3293, Ap	30	135.4	13.8	298	12	US-09-922-293-3293
Sequence 3292, Ap	31	132.8	13.5	285	12	US-09-922-293-3292
Sequence 13542, A	32	132.6	13.5	601	17	US-10-021-323-13542
Sequence 8682, Ap	33	132.6	13.5	639	17	US-10-021-323-8682
Sequence 1, Appli	34	131.4	13.4	4285	15	US-10-104-580-1
Sequence 3443, Ap	35	130.8	13.3	259	12	US-09-922-293-3443
Sequence 3445, Ap	36	130.2	13.3	265	12	US-09-922-293-3445
Sequence 8899, Ap	37	130.2	13.3	649	17	US-10-021-323-8899
Sequence 10295, A	38	126.6	12.9	900	13	US-10-425-114-10295
Sequence 32218, A	39	126.6	12.9	933	13	US-10-424-599-32218
Sequence 3290, A	40	126.2	12.9	251	12	US-09-922-293-3290
Sequence 26809, A	41	126.2	12.9	1148	13	US-10-425-114-26809
Sequence 3282, Ap	42	124.8	12.7	535	12	US-09-732-627A-3282
Sequence 4580, Ap	43	121	12.3	657	13	US-10-425-114-4580
Sequence 7, Appli	44	121	12.3	10140	15	US-10-094-458A-7
Sequence 12120, A	45	119.4	12.2	779	13	US-10-425-114-12120

ALIGNMENTS

RESULT 1

US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-10-104-580-3

Query Match 31.2%; Score 306.4; DB 15; Length 681;
Best Local Similarity 70.1%; Pred. No. 1.5e-79;
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGAGATTGAATCAAGCTGATCGAAACACCAACAGCAGGTGACC 60

Db 1 ATGGTCTGTGGAAGATTGAATCAAGAGTCAAGAAACCCCAACAAACAGCAAGTCAAC 60

QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120

Db 61 TACTCGAGAGAGAAATGGTATTTTCAAGAGAGCCCAAGACTCACTGACTTTGTGAT 120
 Qy 121 GCCAAGGTCTCCCTCATTTATGCTCTCGACACTTAATAAATGACGAGTATATCAGCCCT 180
 Db 121 GCTAAGGTCTCTCTTATCATGTTTCTCCACACACTAACAAACTCAATGAGTACATTAAGCC 180
 Qy 181 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 Db 181 TCCACATCGAAGAGAGATCTAGATCAATATCAGAACCGCTTTAGGCATAGATCTGTGG 240
 Qy 241 AGGACACACAGAGAGTGTGATGAAGACACCTTGTGGAAGTTGAAGAGATCAACAATAAG 300
 Db 241 GGCACCTCAATACGAGAAATGCAAGAGCACTTGAGGAAGCTGAATGATCAATCAATAG 300
 Qy 301 CTGAGGAGAGATCAGGAGAGGTTGGCCCATGATCTTAATGGCCCTGAGCTTGGACGAG 360
 Db 301 CTGAGACAGAAATCAGGACAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
 Qy 361 CTGGCTTCTCTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CTGGCGGTCTTGAGCAACATATGACTGAAGCCTTGAATGGTGTGCTGGCAGGAAGTAC 420
 Qy 421 CATGTGATCAAACTCAGCGAGAGACCAAGAGAGAGTTAAGAACTTGGAGCAAGA 480
 Db 421 CATGTGATCAAAACACAAAACGAACTTACAGGAGAGAGTTGAAGAACTTGGAGGAGAG 480
 Qy 481 AGAGGAACATGCTGCATGCTATTTTGACGAGAGAGAGCGCGGAGGATCCACAGTAT 540
 Db 481 CATGGAAACCT-----CTTGATGGAATATGAAGCAAACTAGAGGATCGACAGTAT 531
 Qy 541 GGTATGAGACAAATGAGGAGAGACTAGCAATCTGCACTTGCATTTGCAATGTCAAAATGGGCGAAT 600
 Db 532 GGTATGAGCAAT-----GAAGTGTGCTTTGCACTTGCATTTGCAAAATGGGCTTCC 579
 Qy 601 AACTGTGACACTTCCACCTCCACCCCTAACCTCCACCAC 642
 Db 580 AACCTTATGATTCGCTGCTGATCAGGGCACAACACCAC 621

RESULT 2

US-10-104-580-2
 ; Sequence 2, Application US/10104580
 ; Publication No. US20030033628A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strauss et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; TITLE OF INVENTION: poplar and other plant species.
 ; FILE REFERENCE: 62486
 ; CURRENT APPLICATION NUMBER: US/10/104,580
 ; CURRENT FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: 09/410,464
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 09/287,700
 ; PRIOR FILING DATE: 1999-04-06
 ; PRIOR APPLICATION NUMBER: 60/080,851
 ; PRIOR FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 946
 ; TYPE: DNA
 ; ORGANISM: Populus balsamifera subsp. trichocarpa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(684)
 US-10-104-580-2

Query Match 31.2%; Score 306.4; DB 15; Length 946;
 Best Local Similarity 70.1%; Pred. No. 1.9e-79;
 Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

Db 1 ATGGGTCTGGAGAGATTGAAATCAAGAGATCGAAACCCCAACAGGCAAGTCACC 60
 Qy 61 TACTCCAGAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCCTTCTCTGTGAT 120
 Db 61 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACITTTGTGAT 120
 Qy 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAAACACTAAATAAATGACGAGTATATCAGCCCT 180
 Db 121 GCTAAGGTCTCTCTTATCATGTTTCTCCACACACTAACAACTCAATGAGTACATTAAGCC 180
 Qy 181 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 Db 181 TCCACATCGAAGAGAGATCTAGATCAATATCAGAACCGCTTTAGGCATAGATCTGTGG 240
 Qy 241 AGGACACACAGAGAGTGTGATGAAGACACCTTGTGGAAGTTGAAGAGATCAACAATAAG 300
 Db 241 GGCACCTCAATACGAGAAATGCAAGAGCACTTGAGGAAGCTGAATGATCAATCAATAG 300
 Qy 301 CTGAGGAGAGATCAGGAGAGGTTGGCCCATGATCTTAATGGCCCTGAGCTTGGACGAG 360
 Db 301 CTGAGACAGAAATCAGGACAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
 Qy 361 CTGGCTTCTCTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CTGGCGGTCTTGAGCAACATATGACTGAAGCCTTGAATGGTGTGCTGGCAGGAAGTAC 420
 Qy 421 CATGTGATCAAACTCAGAGCGGAGACCAAGAGAGAGTTAAGAACTTGGAGCAAGA 480
 Db 421 CATGTGATCAAAACACAAAACGAACTTACAGGAGAGAGTTGAAGAACTTGGAGGAGAG 480
 Qy 481 AGAGGAACATGCTGCATGCTATTTTGACGAGAGAGAGCGCGGAGGATCCACAGTAT 540
 Db 481 CATGGAAACCT-----CTTGATGGAATATGAAGCAAACTAGAGGATCGACAGTAT 531
 Qy 541 GGTATGAGACAAATGAGGAGAGACTAGCAATCTGCACTTGCATTTGCAATGTCAAAATGGGCGAAT 600
 Db 532 GGTATGAGCAAT-----GAAGTGTGCTTTGCACTTGCATTTGCAAAATGGGCTTCC 579
 Qy 601 AACTGTGACACTTCCACCTCCACCCCTAACCTCCACCAC 642
 Db 580 AACCTTATGATTCGCTGCTGATCAGGGCACAACACCAC 621

RESULT 3

US-10-425-114-12758
 ; Sequence 12758, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 12758
 ; LENGTH: 1050
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 701209467_FLI
 US-10-425-114-12758

Query Match 26.3%; Score 257.8; DB 13; Length 1050;
 Best Local Similarity 67.4%; Pred. No. 4.8e-65;
 Matches 431; Conservative 0; Mismatches 187; Indels 21; Gaps 4;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCGAGTGACC 60
DB |||||
QY 58 ATGGCTCGAGCAAGATTGAGATAAAGTTGATTGAGAAACCCACCAACAGGCAAGTCACT 117
DB |||||
QY 61 TACTCCAGAGAGAGAAATGGAGTCTTCAAGAGGCTCAGAGCTCACCCTTCTCTGTGAT 120
DB |||||
QY 118 TACTCCAGAGAGAGAAATGGAGTCTTCAAGAAAGCTCATGAATCAGTGTCTCTGTGAT 177
DB |||||
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAAACACTAATAAAATGACAGATATATCAGCCCT 180
DB |||||
QY 178 GCCAAGGTCTTCATTCATCATGTTCTCTTAAACAAACAAAGATGATGAATACATTAGCCCT 237
DB |||||
QY 181 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 237
DB |||||
QY 238 GGCCTCAGCAAAAGAGATCATTTGATCAGTATCAGAAAGACTTTGGGGGATATTTGATCTG 297
DB |||||
QY 238 TGGAGGACACACGAGGAGTCCGATGAAAGACACCTTTGTGGAAGTTGAAAGAGATCAACAAT 297
DB |||||
QY 298 TGGGCTTCTCACTATGAGAAAATGCTTGAAAACCTTGAAGAGCTGATAGATATTAACAA 357
DB |||||
QY 298 AAGCTGAGGAGAGATCAGGAGAGGTT-----GGGCCATGATCTAAATGGCCTGAGC 351
DB |||||
QY 358 AAGCTCAGAAACAGATCAGGATAGGATAGGAGGTTTGGACATGAGCAGCATGAGC 417
DB |||||
QY 352 TTTGACGAGTGGCTTCTCTTGAGATGAGATGAGTCTTCTTGGATGCCATACGTCAA 411
DB |||||
QY 418 TTCCAGCAACTGCCACTCTTGAAGAGATTTGGTTTCTTCCATAGGGAATAACAGAA 477
DB |||||
QY 412 AGGAAGTACCATGTGATCAAACTCAGACGAGACCAACAGAGAGAGGTTAAGAACTTG 471
DB |||||
QY 478 CGAAAGTTCCACGTGATCAAAACACGAGCTGATACCTGCGAGGAAAAGGTTAAAGCCTG 537
DB |||||
QY 472 GAGCAAGAGAGAAACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 531
DB |||||
QY 538 GAGCAGATGAATAGAGATCTGCTG-----TTTGAACCTGAAAGAGTGGGATCCAT 588
DB |||||
QY 532 CCACAGTATGTTATGAGGACAAATGAGGAGACTTACGAATCTGCATCTGCAATGTCAAAT 591
DB |||||
QY 589 CCACAAATTTATTT---TGCAGATGAAGAGACAGGAAATCAGCAGTTGCACTGGCCAA 645
DB |||||
QY 592 GGGCGGAATAACTGTGATCACTTTCCACCTCCACCAACCT 630
DB |||||
QY 646 GGCCTCCACCTGTATGGTCTGCTGATCAGCAGCACT 684
DB |||||

RESULT 4

US-10-425-114-15025
; Sequence 15025, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15025
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-050-F6_FLI
US-10-425-114-15025

Query Match 25.7%; Score 252.4; DB 13; Length 1231;
Best Local Similarity 71.5%; Pred. No. 2.1e-63;
Matches 363; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCGAGTGACC 60
DB |||||
QY 264 ATGGCTCGTGGCAAGATTGAGATAAAGTTGATTGAGAAACCCACCAACAGGCAAGTCACT 323
DB |||||
QY 61 TACTCCAGAGAGAGAAATGGAGTCTTCAAGAGGCTCAGAGCTCACCCTTCTCTGTGAT 120
DB |||||
QY 324 TACTCCAGAGAGAGAAATGGAGTCTTCAAGAAAGCTCATGAATCAGTGTCTCTGTGAT 383
DB |||||
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAAACACTAATAAAATGACAGATATATCAGCCCT 180
DB |||||
QY 384 GCCAAGGTCTTCATTCATCATGTTCTCTTAAACAAACAAAGATGATGAATACATTAGCCCT 443
DB |||||
QY 181 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 237
DB |||||
QY 444 GGCCTCAGCAAAAGAGATCATTTGATCAGTATCAGAAAGACTTTGGGGGATATTTGATCTG 503
DB |||||
QY 238 TGGAGGACACACGAGGAGTCCGATGAAAGACACCTTTGTGGAAGTTGAAAGAGATCAACAAT 297
DB |||||
QY 504 TGGCATTCTCACTATGAGAAAATGCTTGAAAACCTTGAAGAGCTGAAAGATATTAACAAT 563
DB |||||
QY 298 AAGCTGAGGAGAGATCAGGAGAGGTT-----GGGCCATGATCTAAATGGCCTGAGC 351
DB |||||
QY 564 AAGCTCAGGAGACAGATCAGGATAGGATAGGAGGCTTGGACATGAGCAGCATGAGC 623
DB |||||
QY 352 TTTGACGAGTGGCTTCTCTTGAGATGAGATGAGTCTTCTTGGATGCCATACGTCAA 411
DB |||||
QY 624 TTCCAGCAACTGCCACTCTTGAAGAGATATGTTTTCATCATTAGGGAATAACGGAA 683
DB |||||
QY 412 AGGAAGTACCATGTGATCAAACTCAGACGAGACCAACAGAGAGAGGTTAAGAACTTG 471
DB |||||
QY 684 CGAAAGTTTCACTGATCAAAACCTCGAGTGTGATGATGATGATGATGATGATGATGATGAT 743
DB |||||
QY 472 GAGCAAGAGAGAGAAACATGCTGATG 499
DB |||||
QY 744 AAGCAGATGAATGGAATCTGCTGCTTG 771
DB |||||

RESULT 5

US-10-425-114-11957
; Sequence 11957, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11957
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701148021_FLI
US-10-425-114-11957

Query Match 25.5%; Score 250.8; DB 13; Length 1212;
Best Local Similarity 71.3%; Pred. No. 6.2e-63;
Matches 362; Conservative 0; Mismatches 137; Indels 9; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCGAGTGACC 60
DB |||||
QY 232 ATGGCTCGTGGCAAGATTGAGATAAAGTTGATTGAGAAACCCACCAACAGGCAAGTCACT 291
DB |||||
QY 61 TACTCCAGAGAGAGAAATGGAGTCTTCAAGAGGCTCAGGAGCTCACCCTTCTCTGTGAT 120
DB |||||

QY 361 CTGGCTTCTCTGACGATGAGATCGATCTTCTTGGATGCCATACGTCAAGGAGTAC 420
Db 387 CTAAGCTCTCTGAGGAAGAAATGGACAAGCGCCCAAGGTTGTTCTGTAGCGTAAGTAT 446
QY 421 CATGTGATCAAACTCAGACGGAGACCAACAAGAAGGTTAAGAACTTTGAGCAAGA 480
Db 447 AAGGTGATACAAATCAGATTGACACCACAGGAGAAAGTTTAAACGAGAAAGAGTG 506
QY 481 AGAGAAACATGCTGATGCTATTTTGCAGGAGACCGCGGAGGATCCACAGTAT 540
Db 507 CACAACAGATCTCTGCA-----TGACTTGGATGCAAAAGCAGAGATCCACGTTTT 557
QY 541 GGTATGAGCAATGAGGAGATACGAATCTGCACTTTCATTTGCAAAATGGGGCAAT 600
Db 558 GCATTGATAGTAATGAGGGGATGACGATCTGTGATCGGATTCACAAATTTAGGTCCA 617
QY 601 AACTTGTACACTTCCACCTCCACC 625
Db 618 CGCATGTTTCGATTGACGCTACAGC 642

RESULT 8

US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C. C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(644)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-013-Q1-K6-F12
US-10-021-323-8631

Query Match 24.3%; Score 238.4; DB 17; Length 644;
Best Local Similarity 66.2%; Pred. No. 1.9e-59;
Matches 344; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
QY 1 ATGGCGGCGGGAAGATTGAAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 32 ATGCTCGAGGAAGATCCAGATCAAGCTGATAGAACTCGACCAACAGCGAAGTCAAG 91
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGCTCAGAGCTCACCCTTCTCTGTGAT 120
Db 92 TATTCGAGAGAGAAACGGCTTTTCAAGAAAGCTAATGAACCTTACAGTTCTTTGCGAT 151
QY 121 GCCAAGGTCTCCCTATTATCTCTCCACACTAATAAATGACAGAGTATATCAGCCCT 180
Db 152 GCTAGATTTCGATCATCACTTTTCCACTACTGTTAACTCCATGATTTATCAGCCCT 211
QY 181 ACCACTAGCAAGAGATGATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240
Db 212 TCCACCAACGAAGCAAGTAATTGATCAGTACCAAGAAACCTTTGGGGATCGATCTGG 271
QY 241 AGGACACAGAGGAGTGCATGAAGACACCTTTGGAAGTTGAAGAGATCAACAATAAG 300
Db 272 AACACCCACTATGAGAAATCAAGAGAGCAGTTGAAGCAGCTGAAAGAGGTAAACAGAAC 331

QY 301 CTGAGAGAGAGATCAGGACGAGGTTGGCCATGATCTAAATGGCCTGAGCTTTGACGAG 360
Db 332 CTGCCCAAGAGATTTAGAGAGAGATGGCGGACTCTTTGAATGATTTGAGGATCGAAGAT 391
QY 361 CTGGCTTCTCTTTCAGATGAGATGAGTCTTCTTTGGAATGCCATACGTCAAAGGATAC 420
Db 392 CTTCGTGCTTTTGGAAACAAGAAATGAGAGACTCTGTCACTCTTATTTCGTGATAGAAAGTAT 451
QY 421 CATGTGATCAAACTCAGACGGAGACCAACAGAGAGAGGTTAAGAACTTTGAGCAAGA 480
Db 452 COTGTTCTTCTCAACAGATCGATACCTTCCAGAAAAAGGTGAGGAATGTGGAAGAGATA 511
QY 481 AGAGAAACATGCTGATGGCTATTTTGCACGAGGAGCAG 520
Db 512 CACAAAATCTCTTACATGAACCTGGAATCCCTGAAAGAG 551

RESULT 9

US-10-425-114-10670
; Sequence 10670, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10670
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700958586_FLI
US-10-425-114-10670

Query Match 23.6%; Score 231.8; DB 13; Length 871;
Best Local Similarity 62.4%; Pred. No. 2.1e-57;
Matches 384; Conservative 0; Mismatches 222; Indels 9; Gaps 1;
QY 11 GGAAGATTGAAATCAAGCTGATCGAAACCAACAGGAGGTGACCTACTCTCAAGA 70
Db 1 GAAAGATCCAGATCAAGAGGATAGAGAACACCACCAACCGCCAGGTCACTTATTCTAAAC 60
QY 71 GAAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCCTTCTCTGTGATGCCAGGTCT 130
Db 61 GACGGAATGGCCTTTTCAAGAAAGGCCAAGAGCTCACCCTTCTATGCGATGCCAGGT 120
QY 131 CCTCATTTATGCTCTCCAACTAATAAATGCAGAGTATATCAGCCCTACCTACGAG 190
Db 121 CTATTATTATGTTCTCCAGCACTGGGAACTCCAGAGTACATCAGCCCTCCACTCAA 180
QY 191 CCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
Db 181 CAAAGCAGTTCTTCGATCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 240
QY 251 AGGAGTCGATGAAGACACCTTTGTGGAAGTTTCAAGAGATCAACAATAGCTGAGGAG 310
Db 241 ACAGAAATGACAGAGAACTTTGAAGAACTCAAGAGATGTAATAGGATCTTCGTAAGG 300
QY 311 AGATCAGGAGAGGTTGGGCCATGATCTAAATGGCTGAGTTTGAAGAGTGGCTTCTC 370
Db 301 AGATTAGGAGAGGATGGGAGATTGTCTGAACGATCTGGGCATGGAAGATCTCAAGCTCC 360
QY 371 TTGACGATGAGATGAGTCTTCTTGGATGCCATAGCTCAAGAGAGTACCATGTGATCA 430
Db 361 TTGAGGAAGAAATGGAACAGGCCCGCAAGGTTGTTCTGTAACGTAAGTATAAGGTGATAA 420

Qy 481 AGAGGAAACATGCTGCATG 499
Db 481 TACAAGAACCTGCAGCAGG 499

RESULT 12

US-10-425-114-13190
; Sequence 13190, Application US/10425114
; Publication No. US2004003488A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 13190

; LENGTH: 2237

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: jC-gmfl02220148g09_FLI

US-10-425-114-13190

Query Match 19.8%; Score 194.6; DB 13; Length 2237;
Best Local Similarity 66.7%; Pred. No. 3.8e-46;
Matches 278; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 109 ATGGCTAGAGAAAGATCCAGATCAAGAGGATAGAGAAACCAACCAACCGCCAGGTCACT 168

Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGCTCAGAGGCTCACCGTTCTCTGTGAT 120
Db 169 TACTCTAAACACCGGAATGGCCCTTTCAAGAAGCCAAACAGGCTTACCGTTCTCTGGAT 228

Qy 121 GCCAAGTCTCCCTCATTATGCTCTCCAACTAATAAATGCAAGATATATCAGCCCT 180
Db 229 GCCAAGTTCTATTATTAATGTTCTCCAGCACTGGAAAACCTCCACAGTACATCAGCCCT 288

Qy 181 ACCCTAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 289 TCCACCTCAACAAAGCAGTTCTTCCGATCAATACAGATGACTCTGGAGTTGATCTCTGG 348

Qy 241 AGGACACAGGAGTGGATGAAAGACACCTTGTGGAGTTGAAAGAGATCAACAATAAG 300
Db 349 AACTCTATTACGAGATATGCAAGAGAACTTGAAGAACTGAAAGAGTGAATAGGAAT 408

Qy 301 CTGAGGAGAGATCAGCAGAGGTTGGCCATGATCTAAATGGCCTTGAGCTTTGACGAG 360
Db 409 CTTCGTAAGGAGATTAGGACAGAGATGGAGATTCTCTGAACGAGCTGGGCATGGAAGAT 468

Qy 361 CTGGCTTCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
Db 469 CTCAAGCTCTTGAAGAAATGGACAGCCGCCAAGGTTGTTCTGTAGCGTTAG 525

RESULT 13

US-10-424-599-120795

; Sequence 120795, Application US/10424599

; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 120795

; LENGTH: 2718

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1

US-10-424-599-120795

Query Match 19.6%; Score 192; DB 13; Length 2718;
Best Local Similarity 65.8%; Pred. No. 2.6e-45;
Matches 279; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 126 ATGGCTCGAGGAAGATCCAGATCAAGAGGATAGAGAACCAACCAACCGCCAGGTCACT 185

Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGGCTCAGAGCTCACCGTTCTCTGTGAT 120
Db 186 TATTCTAAACGACGGAATGGCCCTTTTCAAGAAGGCCAACGAGCTCACCGTTCTATGCGAT 245

Qy 121 GCCAAGTCTCCCTCATTATGCTCTCCAACTAATAAATGCAAGATATATCAGCCCT 180
Db 246 GCCAAGTTCTATTATTAATGTTCTCCAGCACTGGAAAACCTCCAGAGTACATCAGCCCC 305

Qy 181 ACCCTAGCACCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 306 TCCACCTCAACAAAGCAGTTCTTCGATCAGTACCAGATGACTCTAGGAGTGCATCTCTGG 365

Qy 241 AGGACACAGGAGTGGATGAAAGACACCTTGTGGAGTTGAAAGAGATCAACAATAAG 300
Db 366 AACTCTCAATTACGAAATATGCAAGAGAACTTGAAGAACTCAAGATGTAATAGGAAT 425

Qy 301 CTGAGGAGAGATCAGGACAGAGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAG 360
Db 426 CTTCGTAGGAGATTAGGACAGAGGATGGAGATTCTCTGAACGATCTGGGCATGGAAGAT 485

Qy 361 CTGGCTTCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 486 CTCAAGCTCTTGAAGAAATGGACAGGCCCAAGGTTGTTCTGTAGCGTAGGCTC 545

Qy 421 CATG 424

Db 546 GAGG 549

RESULT 14

US-09-922-293-3294

; Sequence 3294, Application US/09922293

; Publication No. US2004012339A1

GENERAL INFORMATION:

; APPLICANT: Conner, Timothy W.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Liu, Jingdong

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.254

; CURRENT APPLICATION NUMBER: US/09/922,293

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/067,000

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: US 60/069,472

; PRIOR FILING DATE: 1997-12-09

; PRIOR APPLICATION NUMBER: US 60/071,479

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/074,201

; PRIOR FILING DATE: 1998-02-10

; PRIOR APPLICATION NUMBER: US 60/074,282

1	PRIOR APPLICATION NUMBER: US 60/089,811
2	PRIOR FILING DATE: 1998-06-18
3	PRIOR APPLICATION NUMBER: US 60/089,807
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5	PRIOR APPLICATION NUMBER: US 60/089,806
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7	PRIOR APPLICATION NUMBER: US 60/089,813
8	PRIOR FILING DATE: 1998-06-18
9	PRIOR APPLICATION NUMBER: US 60/089,811
10	PRIOR FILING DATE: 1998-06-18
11	PRIOR APPLICATION NUMBER: US 60/089,793
12	PRIOR FILING DATE: 1998-06-18
13	PRIOR APPLICATION NUMBER: US 60/091,405
14	PRIOR FILING DATE: 1998-06-30
15	PRIOR APPLICATION NUMBER: US 60/091,247
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58	PRIOR FILING DATE: 1998-11-18
59	PRIOR APPLICATION NUMBER: US 60/108,996
60	PRIOR FILING DATE: 1998-11-18
61	PRIOR APPLICATION NUMBER: US 09/199,129
62	PRIOR FILING DATE: 1998-11-24
63	PRIOR APPLICATION NUMBER: US 09/210,297
64	PRIOR FILING DATE: 1998-12-08
65	PRIOR APPLICATION NUMBER: US 60/111,981
66	PRIOR FILING DATE: 1998-12-11
67	PRIOR APPLICATION NUMBER: US 60/113,224
68	PRIOR FILING DATE: 1998-12-22
69	PRIOR APPLICATION NUMBER: US 09/229,413
70	PRIOR FILING DATE: 1999-01-12
71	NUMBER OF SEQ ID NOS: 3853
72	SEQ ID NO 3294
73	LENGTH: 407


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; TYPE: DNA
; ORGANISM: Glycine max
US-09-922-293-3294

Query Match      19.5%; Score 191; DB 12; Length 407;
Best Local Similarity 68.7%; Pred.No.1.4e-45;
Matches 263; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCAAGACCAACAGCGAGGTGACC 60
DB 25 ATGCTCGAGGAAGATCCAGATCAAGAGGATAGAGAACCAACCAACCGCCAGGTCACT 84
QY 61 TACTCCAAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGCTCACCCTTCTCTGTGAT 120
DB 85 TATTCTAAACGACGGAATGGCTTTTCAAGAGGCCCAACGAGCTCACCCTTCTATGCGAT 144
QY 121 GCCAAGGTCTCCCTCATTATGTCTCCCAACACTAATAAATGCAACGAGTATATCAGCCCT 180
DB 145 GCCAAGGTCTTATATATATGTCTCCAGACTGGGAACTCCAGAGTACATCAGCCCC 204
QY 181 ACCACTACGACCAAGAGATGTATGATGATATCAGAAAATCTATGGGATCGATCTGTGG 240
DB 205 TCCACCTCAACAAAGCAGTCTTTCGATCAGTACCAAGATGACTCTAGGAGTCGATCTCTGG 264
QY 241 AGGACACAGGAGTCTGATGAAAGACACCTTGTGGAGTTGAAAGAGATCAACAATAAG 300
DB 265 AACTCTTATACGAGAATATGCAAGAGAACTTGAAGAACTCAAAGATGTAATAGGAAT 324
QY 301 CTGAGGAGAGATCAGGACAGAGTTGGGCCATGATCTAAATGCCCTTGTGACGAG 360
DB 325 CTTCGTAAGGAGATTAGCGAGAGATGGGAGATGTTCTGAACGATCTGAGCATGGAAGAT 384
QY 361 CTGCGCTTCTTGTGAGATGAGAT 383
DB 385 CTCAGCTCTCTTGGAGGAAT 407

RESULT 15
US-09-922-293-14
; Sequence 14, Application US/09922293
; Publication No. US20040123339A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Transcription in Plants
; FILE REFERENCE: 16517.254
; CURRENT APPLICATION NUMBER: US/09/922.293
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: US 60/069,472
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: US 60/071,479
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; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/075,462
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/074,789
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 60/075,459
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; PRIOR APPLICATION NUMBER: US 60/075,461
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;; PRIOR APPLICATION NUMBER: US 09/210,297
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;; PRIOR APPLICATION NUMBER: US 60/111,981
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/113,224
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: US 09/229,413
;; PRIOR FILING DATE: 1999-01-12
;; NUMBER OF SEQ ID NOS: 3853
;; SEQ ID NO 14
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-922-293-14

Query Match 19.0%; Score 186.4; DB 12; Length 425;
Best Local Similarity 65.2%; Pred. No. 3.4e-44;
Matches 274; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
QY 3 GCGCGCGGGAAGTGAATCAAGCTGATCGAAACCCAGACCCAGGAGGTGACCTA 62
Db 1 GCGGAGAGGGAAGATCCAGATCAAGAGGATAGAGAACCCAGACAAACAGACAAAGTGCCTA 60
QY 63 CTCACAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGATGC 122

Db 61 TTCAAAGAGAGAAATGGTTTATTCAAGAAAGCATGAGCTCAGGTTTTGTGTGATGC 120
QY 123 CAAGGTCTCCCTCATTTATGCTCTCAACACACTAATAAATGCAAGAGTATATCAGCCCTAC 182
Db 121 TAGGGTTTCGATTATCATGTTCTTAGCTCCAAAGAGCTTCATGAGTATATCAGCCCTAA 180
QY 183 CACTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGGATCGATCTGTGGAG 242
Db 181 CACCACAAACGAGGAGATCGTAGATCTGTACCAAACTATTTCTGATGTCGATGTTTGGGC 240
QY 243 GACACACGAGGAGTCGATGAAGACACCTTGTGAAGTTGAAGAGATCAACAATAGCT 302
Db 241 CACTCAATATGAGCGAATGCAAGAAACCAAGAGGAAACTGTTGGAGACAAATAGAAATCT 300
QY 303 GAGGAGAGAGATCAGGCAAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAGCT 362
Db 301 CCGGACTCAGATCAAGCAGAGGCTAGGTGAGTGTGGACGAGCTTGACATTCAGGAGCT 360
QY 363 GCTTCTCTTGCAGATGAGATGCGAGTCTTCTTGGATGCCATAGCTCAAGAGAGTACCA 422
Db 361 GCGTCGTCTTGAGGATGAATGGAACACATTTCAAACTCGTTCCGAGCGCAAGTTCAA 420

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
6376.765 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306.4	31.2	681	4	US-09-410-464-3
2	306.4	31.2	945	4	US-09-410-484-2
3	131.4	13.4	4285	4	US-09-410-464-1
4	100.6	10.2	1180	2	US-08-867-087B-16
5	96.8	9.9	1059	2	US-08-867-087B-14
6	94.4	9.6	1345	1	US-08-592-214A-7
7	94.4	9.6	1345	3	US-08-659-188-7
8	94.4	9.6	1345	3	US-08-655-227-7
9	94.4	9.6	1345	3	US-08-655-241-7
10	94.4	9.6	1345	3	US-09-149-976-7
11	94.4	9.6	1345	4	US-09-398-326-7
12	94	9.6	1043	2	US-08-867-087B-12
13	93.6	9.5	945	2	US-08-485-981-9
14	93.6	9.5	945	2	US-08-867-087B-10
15	93.2	9.5	779	1	US-08-592-214A-9
16	93.2	9.5	779	3	US-08-659-188-9
17	93.2	9.5	779	3	US-08-655-227-9
18	93.2	9.5	779	3	US-08-655-241-9
19	93.2	9.5	779	3	US-09-149-976-9
20	93.2	9.5	779	4	US-09-398-326-9
21	93.2	9.5	5855	1	US-08-592-214A-20
22	93.2	9.5	5855	2	US-09-149-976-20
23	91	9.3	1027	2	US-08-867-087B-54
24	89.2	9.1	795	3	US-08-904-284-2
25	87.8	8.9	1141	2	US-08-323-449B-1
26	87.8	8.9	1141	2	US-08-485-981-1
27	87.8	8.9	1141	2	US-08-867-087B-1

ALIGNMENTS

RESULT 1
US-09-410-464-3
; Sequence 3, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-09-410-464-3

Query Match 31.2%; Score 306.4; DB 4; Length 681;
Best Local Similarity 70.1%; Pred. No. 2.7e-76;
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

Qy 1 ATGGCGCGGGAAGATTCAAAATCAAGCTGATCGAAACCAGACCAACAGGAGGTGACC 60
Db 1 ATGGGTCTGGGAAGATTGAAATCAAGAAGATCGAAACCAGACCAACAGGAGGTGACC 60

Qy 61 TACTCAAGAGAAGAAATCGGATCTTCAAGAAGGTTCAGAGCTCACCTTCTTGAT 120
Db 61 TACTCAAGAGAAGAAATCGGATCTTCAAGAAGGTTCAGAGCTCACCTTCTTGAT 120

Qy 121 GCCAAGTCTCCTCATTTATGCTCCACACTATAAATGCACAGTATATCAGCCCT 180
Db 121 GCTAAGTCTCTTATCATGTCTCCAACTTACAACTCAATGAGTATATGCCCC 180

Qy 181 ACCACTACCAACAAGATGTATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 181 TCCACATCGACAAGAAGATCTACGATCAATATCAGAACGCTTAGGCATAGATCTGTGG 240

Qy 241 AGGACACAGAGAGTCTGATGAAGACACTTGTGGAAGTTGAAGAGATCAACAATAG 300
Db 241 GGCACTCAATACAGAGAAATGCAAGAGCACCTTGAGGAGCTGATGATATCAATCAAG 300

QY 301 CTGAGGAGAGATCAGGAGAGGTTGGCCCATGATCTAAATGCGCTGAGCTTTGACGAG 360
DB 301 CTGAGACAGAAATCAGGACAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
QY 361 CTGCGCTTCTTTGACGATGAGATGAGATGAGTCTTCTTTGATGCCATACGTCGCAAGGAGTAC 420
DB 361 CTGCGCGGCTCTTGAGCAACATATGACTGAAGCCTTTGAATGGTGGCTGGCAGCAAGTAC 420
QY 421 CATGTGATCAAACTCAGCGGACCAACAGAGAGGTTAAGACTTTGGAGCAAGA 480
DB 421 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480
QY 481 AGAGAAACATGCTGCTGCTATTTTGACCAAGGAGCAGCGCGGAGGATCCACAGTAT 540
DB 481 CATGGAACCTT-----CTTGATGGAATATGAACCAAACTAGAGGATCGACAGTAT 531
QY 541 GGTATGAGGACATGAGGAGACTACGATCTGCATCTGCATTTGCAATGGGGCAAT 600
DB 532 GGTATTAGTGACAAT-----GAAGCTGCTGTTGCATCTGCAATGGGGCTTCC 579
QY 601 AACTTGTACACTTTCCACCTCCACCCCTAACTCCACCAC 642
DB 580 AACCTCTATGATTCGCGCTGCATCAGGGCAGCAACACCAC 621

RESULT 2
US-09-410-464-2
; Sequence 2, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-09-410-464-2

Query Match 31.2%; Score 306.4; DB 4; Length 946;
Best Local Similarity 70.1%; Pred. No. 3.2e-76;
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGAGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60
DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAGGCAAGTCAACC 60
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGTCTACCGTTCTCTGTGAT 120
DB 61 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 120
QY 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACTAAATAAATGACGAGTATATCAGCCCT 180
DB 121 GCTAAGGTCTCTTATCATGTTCTCCACACTAACTCAACTCAATGAGTACATAGCCCC 180
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTG 240
DB 181 TCCACATCGACAAAGAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240
QY 241 AGGACACACGAGGATCGATGAAGACACCTTGTGGAAGTTGAAGAGATCAACAATAG 300

DB 241 GGCACTCAATACGAGAAAATCAAGAGACACTTGAGGAAGCTGAATGATCAATCATATAAG 300
QY 301 CTGAGAGAGAGATCAGGACAGAGTTGGCCCATGATCTAAATGCGCTTGGAGCTTTGACGAG 360
DB 301 CTGAGACAGAAATCAGGACAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
QY 361 CTGGGCTTCTTTGACGATGAGATGAGTCTTCTTTGATGCCATACGTCGCAAGGAGTAC 420
DB 361 CTGCGCGGCTCTTGAGCAACATATGACTGAAGCCTTTGAATGGTGGCTGGCAGGAGTAC 420
QY 421 CATGTGATCAAACTCAGACGAGACCAACAGAGAGGTTAAGAACTTTGGAGCAAGA 480
DB 421 CATGTGATCAAAACACAAACGAAACCTTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480
QY 481 AGAGAAACATGCTGCTGCTATTTTGACCAAGGAGCAGCGCGGAGGATCCACAGTAT 540
DB 481 CATGGAACCTT-----CTTGATGGAATATGAACCAAACTAGAGGATCGACAGTAT 531
QY 541 GGTATGAGGACATGAGGAGACTACGATCTGCATCTGCATTTGCAATGGGGCAAT 600
DB 532 GGTATTAGTGACAAT-----GAAGCTGCTGTTGCATCTGCAATGGGGCTTCC 579
QY 601 AACTTGTACACTTTCCACCTCCACCCCTAACTCCACCAC 642
DB 580 AACCTCTATGATTCGCGCTGCATCAGGGCAGCAACACCAC 621

RESULT 3
US-09-410-464-1
; Sequence 1, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-1

Query Match 13.4%; Score 131.4; DB 4; Length 4285;
Best Local Similarity 76.1%; Pred. No. 8.8e-27;
Matches 162; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGGCGCGGAGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60
DB 2001 ATGGTCTGTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAGGCAAGTCAACC 2060
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGTCTACCGTTCTCTGTGAT 120
DB 2061 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 2120
QY 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACTAAATAAATGACGAGTATATCAGCCCT 180
DB 2121 GCTAAGGTCTCTTATCATGTTCTCCACACTAACTCAACTCAATGAGTACATAGCCCC 2180
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTAT 213
DB 2181 TCCACATCGTACGTATATCTCGTATCATGTTTCT 2213

RESULT 4
US-08-867-087B-16

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; Sequence 16, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-867-087B-16

Query Match 10.2%; Score 100.6; DB 2; Length 1180;
Best Local Similarity 68.5%; Pred. No. 2e-18;
Matches 139; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1 ATGCGCGCGGGAAGATTGAATCAAGTGTATCGAAACACAGACCAACAGGAGGTGACC 60
Db 110 ATGGGAGAGGAGGAGGTGAGCTGAAGAGGATCGAGACACAGATCAACAGGAGGTGACG 169
Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGCTCAGAGCTCAGGTTCTCTGTGAT 120
Db 170 TTCCGGAAGCGGAGAAATGGGCTGCTCAAGAAGCGTACGAGTCTCCGTGCTCGAC 229
Qy 121 GCCAAGGTCTCCCTCATTTATCTCTCAACACTATAATAATGACAGATATATCAGCCCT 180
Db 230 GCCAGGTGCGCCCTCATCTCTTCTCAACCGGCGAAGCTCTACGAGTTCTGCGCGGC 289
Qy 181 ACCACTACGACCAAGATGTA 203
Db 290 CAAAGCATGACCAAGACTTTTGA 312

RESULT 5
US-08-867-087B-14
; Sequence 14, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung

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; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-867-087B-14

Query Match 9.9%; Score 96.8; DB 2; Length 1059;
Best Local Similarity 68.4%; Pred. No. 2.2e-17;
Matches 134; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1 ATGCGCGCGGGAAGATTGAATCAAGTGTATCGAAACACAGACCAACAGGAGGTGACC 60
Db 98 ATGGGAGAGGAGGAGGTGAGCTGAAGAGGATCGAGACACAGATCAACCGGAGGTGACG 157
Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACGTTCTCTGTGAT 120
Db 158 TTCCGCAAGAGGAGGAGATGGCTGCTCAAGAAGCGGTACGAGTCTCCGTCTCTGCGAC 217
Qy 121 GCCAAGGTCTCCCTCATTTATCTCTCAACACTATAATAATGACAGATATATCAGCCCT 180
Db 218 GCCAGGTGCGCCCTCATCTCTTCTCAACCGGCGAAGCTCTACGAGTTCTGCGAGCC 277
Qy 181 ACCACTACGACCAAGA 196
Db 278 CAGAGCATGACTAAAA 293

RESULT 6
US-08-592-214A-7
; Sequence 7, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin P.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1"
US-08-592-214A-7

Query Match 9.6%; Score 94.4; DB 1; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAATAACCAAGCAACAGGCGAGGTGACC 60
DB 149 ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAATAACCAAGCAACAGGCGAGGTGACC 208
QY 61 TACTCCAGAGAGAGAAATGGGATCTTCAAGAGCTCAGGAGTCCACCGTTCTCTGTGAT 120
DB 209 TTCTCCAGGCGCGGGAAGCGGCTGCTCAAGAGCGGCAAGAGATCTCCGTTCTCTCGAT 268
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCCAACACTAATAAATGACGAGTATATCAGCCCT 180
DB 269 GCCGAGTCCGCGTCATCGTCTTCTCCCAAGGCAAGCTTACGAGTACGCCACCGAC 328
QY 181 ACCACTAGCAGCAAGAGTAT 200
DB 329 TCCCGCATGGACAAATTTCT 348

RESULT 7
US-08-592-188-7
Sequence 7, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1."
US-08-659-188-7

Query Match 9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAATAACCAAGCAACAGGCGAGGTGACC 60
DB 149 ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAATAACCAAGCAACAGGCGAGGTGACC 208
QY 61 TACTCCAGAGAGAGAAATGGGATCTTCAAGAGCTCAGGAGTCCACCGTTCTCTGTGAT 120
DB 209 TTCTCCAGGCGCGGGAAGCGGCTGCTCAAGAGCGGCAAGAGATCTCCGTTCTCTGGAT 268
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCCAACACTAATAAATGACGAGTATATCAGCCCT 180
DB 269 GCCGAGTCCGCGTCATCGTCTTCTCCCAAGGCAAGCTTACGAGTACGCCACCGAC 328
QY 181 ACCACTAGCAGCAAGAGTAT 200
DB 329 TCCCGCATGGACAAATTTCT 348

RESULT 8
US-08-659-227-7
Sequence 7, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALAL Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1."
US-08-655-227-7

Query Match 9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 149 ATGCGCGCGGAGATGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 208
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTGAT 120
Db 209 TTCTCCAGCGCGGACGGCTGCTCAAGAGGCGCACGAGATCTCCGTCCTCTGCGAT 268
QY 121 GCCAAGTCTCCCTCATATGCTTCCCAACTATATAAATGACGAGTATATACGCCCT 180
Db 269 GCCAGGTCCGCTCATGCTTCTCCCAAGGCAAGCTCTACGAGTACGCCACCGAC 328
QY 181 ACCACTACGACCAAGAGTAT 200
Db 329 TCCCGCATGGACAAAATTCT 348

RESULT 9
US-08-655-241-7
Sequence 7, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1."
US-08-655-241-7

Query Match 9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 149 ATGCGCGCGGAGATGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 208
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTGAT 120
Db 209 TTCTCCAGCGCGGACGGCTGCTCAAGAGGCGCACGAGATCTCCGTCCTCTGCGAT 268
QY 121 GCCAAGTCTCCCTCATATGCTTCCCAACTATATAAATGACGAGTATATACGCCCT 180
Db 269 GCCAGGTCCGCTCATGCTTCTCCCAAGGCAAGCTCTACGAGTACGCCACCGAC 328
QY 181 ACCACTACGACCAAGAGTAT 200
Db 329 TCCCGCATGGACAAAATTCT 348

RESULT 10
US-09-149-976-7
Sequence 7, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/592,214
 FILING DATE: 26-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 3291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1345 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 149..968
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..1345
 OTHER INFORMATION: /note= "product = Zea mays APl"

US-09-149-976-7
 Query Match 9.6%; Score 94.4; DB 3; Length 1345;
 Best Local Similarity 67.0%; Pred. No. 1.2e-16;
 Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACACAGACCAAGGAGGTGACC 60
 Db 149 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACACAGACCAAGGAGGTGACC 208
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 Db 209 TTCTTCCAAAGCGCGGAGGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGGAT 268
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 Db 269 GCCAAGTCTCCCTCATATGCTTCCCAACTAATAAATGACAGATATATCAGCCCT 328
 QY 181 ACCACTACGACCAAGAGTAT 200
 Db 329 TCCCGCATGGACAAATCT 348

RESULT 11
 US-09-398-326-7
 Sequence 7, Application US/09398326
 Patent No. 6355963
 GENERAL INFORMATION:
 APPLICANT: Yanofsky, Martin F.
 TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
 TITLE OF INVENTION: Reproductive Development and Methods of Making Same
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/398,326
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188
 FILING DATE: 05-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 3739
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1345 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 149..968
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..1345
 OTHER INFORMATION: /note= "product = Zea mays APl."

US-09-398-326-7
 Query Match 9.6%; Score 94.4; DB 4; Length 1345;
 Best Local Similarity 67.0%; Pred. No. 1.2e-16;
 Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACACAGACCAAGGAGGTGACC 60
 Db 149 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACACAGACCAAGGAGGTGACC 208
 QY 61 TACTTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 120
 Db 209 TTCTTCCAAAGCGCGGAGGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGGAT 268
 QY 121 GCCAAGTCTCCCTCATATGCTTCCCAACTAATAAATGACAGATATATCAGCCCT 180
 Db 269 GCCAAGTCTCCCTCATATGCTTCCCAACTAATAAATGACAGATATATCAGCCCT 328
 QY 181 ACCACTACGACCAAGAGTAT 200
 Db 329 TCCCGCATGGACAAATCT 348

RESULT 12
 US-08-867-087B-12
 Sequence 12, Application US/08867087B
 Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: An, Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klarquist
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997


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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-867-087B-12

Query Match          9.6%; Score 94; DB 2; Length 1043;
Best Local Similarity 68.4%; Pred. No. 1.3e-16;
Matches 130; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGGAGATTGAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60
DB 34 ATGGGAGGGGAGAGTTGAGCTGAGCGCATCGAGAACAGATCAACAGGCGAGGTCAAC 93
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCAGCGTCTCTGTGAT 120
DB 94 TTCTCCAGGCCGCCAACGGGCTCTCAAGAGGCCCTACAGAGTGTCTCTGTGAC 153
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTATAATAATGACAGAGTATATCAGCCCT 180
DB 154 GCCGAGGTGGGCTCATCTCTCCAGCGCGGCGAGCTTACAGAGTTGGCGAGCGCC 213
QY 181 ACCACTACGA 190
DB 214 GGCATAACAA 223

RESULT 13
US-08-485-981-9
; Sequence 9, Application US/08485981
; Patent No. 5861542
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND
; TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,981
; FILING DATE: June 7, 1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994

```

```

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-42933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-485-981-9

Query Match          9.5%; Score 93.6; DB 2; Length 945;
Best Local Similarity 67.3%; Pred. No. 1.6e-16;
Matches 132; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGGAGATTGAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60
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QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCAGCGTCTCTGTGAT 120
DB 76 TTGGCTAAGAGAGAAATGGACTTTTGAAAAAGCTTATGAGCTTCTGTGAT 135
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QY 181 ACCACTACGACCAAGA 196
DB 196 TCTAGCATGCTCAAGA 211

RESULT 14
US-08-867-087B-10
; Sequence 10, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123

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REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-867-087B-10

Query Match 9.5%; Score 93.6; DB 2; Length 945;
Best Local Similarity 67.3%; Pred. No. 1.6e-16;
Matches 133; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGATTGAAATCAAGCTGATCGAAACCAAGACCAACAGGCGAGGTGACC 60
Db 16 ATGGGAAGGGGTAGGGTTGAGCTTAAGAGAAATAGAGACAAGATCAACAGGCAAGTGACC 75
QY 61 TACTCCAAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120
Db 76 TTGCTTAGAGAGAAATGAGACTTTTCAAAAAGCTTATGAGCTTCTGTCTTTGTGAT 135
QY 121 GCCAAGTCTCCCTCATATGCTCTCCAACTAAATAAATGCAAGATATATCAGCCCT 180
Db 136 GCTGAGGTTGCTCTCATCATCTTCTCCATAGGGGAAACCTGTACGAGTTCTGCAGTAGC 195
QY 181 ACCACTAGCACCAGA 196
Db 196 TCTAGCATGCTCAAGA 211

RESULT 15
US-08-592-214A-9
Sequence 9, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanoofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 10..775
FEATURE:
NAME/KEY: unsure
LOCATION: 778..779 /note= "N = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "product = Arabidopsis
thaliana CAL"
US-08-592-214A-9

Query Match 9.5%; Score 93.2; DB 1; Length 779;
Best Local Similarity 71.8%; Pred. No. 1.9e-16;
Matches 122; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGATTGAAATCAAGCTGATCGAAACCAAGACCAACAGGCGAGGTGACC 60
Db 10 ATGGGAAGGGGTAGGGTTGAAATTGAGAGGATAGAGAACCAAGATCAATAGACAAGTGACA 69
QY 61 TACTCCAAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120
Db 70 TTCTCGAAAGAGAACTGGTCTTTTGAAGAGAGCTCAGGAGATCTCTGTCTTTGTGAT 129
QY 121 GCCAAGTCTCCCTCATATGCTCTCCAACTAAATAAATGCAAGATATATCAGCCCT 170
Db 130 GCCGAGGTTTCCCTTATTGTCTTCTCCATAAGGGCAAATTGTTCGAGTA 179

Search completed: September 25, 2004, 22:05:12
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 13:15:32 ; Search time 455.966 Seconds
(without alignments)
9149.204 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcggggaagtga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	982	100.0	982	4 AAS00104	Aas00104 Granny Sm
2	306.4	31.2	681	4 AAF85393	Aaf85393 Nucleotid
3	306.4	31.2	946	4 AAF85392	Aaf85392 Nucleotid
4	306.4	31.2	946	6 ABK88485	Abk88485 Poplar pr
5	306.4	31.2	946	8 ACA62518	ACA62518 Poplar ho
6	303.2	30.9	924	3 AAZ57943	Aaz57943 Poplar fl
7	247.2	25.2	989	3 AAC55879	Aac55879 Eucalyptu
8	237	24.1	926	6 AAD42259	Aad42259 Soybean A
9	236.4	24.1	882	2 AAQ51189	Aaq51189 Homeotic
10	227.4	23.2	954	3 AAC51525	Aac51525 Arabidops
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12	225.8	23.0	1170	3 AAC51790	Aac51790 Arabidops
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27	129	13.1	780	6 ABK82086	Abk82086 Novel flo
28	129	13.1	783	6 ABK82087	Abk82087 Novel flo
29	129	13.1	1065	6 ABK82127	Abk82127 DNA encod
30	129	13.1	1065	6 ABK82124	Abk82124 DNA encod
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32	128.2	13.1	4192	3 AAZ57942	Aaz57942 Poplar fl
33	126.2	12.9	1004	3 AAC46623	Aac46623 Zea mays
34	121	12.3	10139	6 ABQ81397	Abq81397 Truncated
35	116.6	11.9	1089	6 AAD42258	Aad42258 Corn AP3
36	110.6	11.3	896	9 ADD55880	Add55880 Thalecres
37	110.6	11.3	947	3 AAC39436	Aac39436 Arabidops
38	106	10.8	446	3 AAC48151	Aac48151 Zea mays
39	106	10.8	495	3 AAC48125	Aac48125 Zea mays
40	105.4	10.7	780	2 AAQ55089	Aaq55089 fbpl cDNA
41	103.4	10.5	909	3 AAC35208	Aac35208 Arabidops
42	101	10.3	560	3 AAC34803	Aac34803 Arabidops
43	100.6	10.2	1181	2 AAV71741	Aav71741 Rice OsmA
44	100.6	10.2	1181	3 AAL44855	Aal44855 Plant flo
45	100.2	10.2	706	3 AAC55965	Aac55965 Eucalyptu

ALIGNMENTS

RESULT 1
ID AAS00104 standard; cDNA; 982 BP.
XX
AC AAS00104;
XX
DT 11-SEP-2003 (revised)
DT 17-MAY-2001 (first entry)
XX
DE Granny Smith apple cDNA encoding MdAP3.
XX
KW Granny Smith apple; MdAP3; seedless fruit; horticulture;
KW accelerated breeding programme; cross pollination; transgenic plant;
KW biennial bearing tendency; codling moth; ss.
XX
OS Malus x domestica; var. Granny Smith.
XX
FH Key Location/Qualifiers
CDS 1..699
FT /*tag= a
FT /product= "MdAP3"
XX
XX WO200117334-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-NZ000176.
XX
PR 07-SEP-1999; 99NZ-00337688.
XX
XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
XX
XX Yao J, Morris BA;
XX WPI; 2001-235145/24.
XX P-RSDB; AAU00187.
XX
XX New genetically modified fruiting plants that does not functionally
XX express MdPI or MdAP3 peptides, useful for producing seedless fruits,
XX specifically apple and its related species.
XX
XX Claim 17; Fig 6; 41pp; English.
XX
XX The sequence encodes Granny Smith apple MdAP3. The invention concerns a
XX fruiting plant that has been genetically modified so that it does not
XX functionally express the MdPI or MdAP3 peptide, producing seedless

CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
 CC may be used to transform fruiting plants, specifically apple and pear.
 CC The polynucleotides may be used in modulating, reducing or eliminating
 CC seed-bearing capacity in fruiting plants, used in horticulture, and in
 CC breeding programmes to monitor the progress in breeding a stable seedless
 CC fruiting plant. The polynucleotides may also be used in programmes for
 CC identifying nucleic acid variants from fruiting plants. They can be used
 CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenics by cross
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 982 BP; 308 A; 203 C; 226 G; 245 T; 0 U; 0 Other;

Query Match 100.0%; Score 982; DB 4; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.8e-252;
 Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGCGCGGAGATTGAATCAAGCTCATCGAAACCCAGACACAGCGAGGTGACC 60
 DB 1 ATGGCGCGCGGAGATTGAATCAAGCTCATCGAAACCCAGACACAGCGAGGTGACC 60
 QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTAT 120
 DB 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTAT 120
 QY 121 GCCAAGTCTCCCTCATATGCTCTCCACACTAATAAATGACAGATATACGCCCT 180
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 QY 181 ACCACTACGACAGAGATATGATGATCTATCAAGAACTATGGGATCGATCTGTGG 240
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 QY 241 AGACACACAGAGAGTCGATGAAGACACCTTTGTGAAGTTGAAGAGATCAACATAAG 300
 DB 241 AGACACACAGAGAGTCGATGAAGACACCTTTGTGAAGTTGAAGAGATCAACATAAG 300
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 QY 361 CTGGCTTCTTTCGACGATGAGATGCGATCTTCTTGATGCCATACGTCAAGGAAGTAC 420
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 QY 421 CATGTGATCAAACTCAGCGGAGACCCACAGAAAGGTTAAGAACTTGGAGCAAGA 480
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 QY 481 AGAGAAACATGTGCTGCTATTTTGGACAGAGACCGCGGAGGATCCACAGTAT 540
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 QY 541 GGTATGAGACAACTGAGGAGATCAGATCTGCACTTGCATTGTCAATGGGCGAAT 600
 DB 541 GGTATGAGACAACTGAGGAGATCAGATCTGCACTTGCATTGTCAATGGGCGAAT 600
 QY 601 AACTTGTACACTTTCACCTCCACCCCTTAACCTCCACCGGAGAGAGCTCGTCCGC 660
 DB 601 AACTTGTACACTTTCACCTCCACCCCTTAACCTCCACCGGAGAGAGCTCGTCCGC 660
 QY 661 TCCTCATTAATCTGATGACAGATCTCCGCTTGTGATCTGATCTGATATGATTA 720
 DB 661 TCCTCATTAATCTGATGACAGATCTCCGCTTGTGATCTGATCTGATATGATTA 720

DB 661 TCCTCATTAATCTGATGACAGATCTCCGCTTGTGATCTGATCTGATATGATTA 720
 QY 721 ATCATCACTAAGTTATATATTAAGTCACTTATTAAGTCTTTTCTCTAAAGTGTGCT 780
 DB 721 ATCATCACTAAGTTATATATTAAGTCACTTATTAAGTCTTTTCTCTAAAGTGTGCT 780
 QY 781 TGGTGACTATCTTTAGGCAAGGATTAGACTGAGTGTGACTCTGAAAACAGATGATAAA 840
 DB 781 TGGTGACTATCTTTAGGCAAGGATTAGACTGAGTGTGACTCTGAAAACAGATGATAAA 840
 QY 841 TATGTGTGTGTGTTTAAATCAATGATAGCACTAAAAAATCCGCGCTTTGCTTGT 900
 DB 841 TATGTGTGTGTGTTTAAATCAATGATAGCACTAAAAAATCCGCGCTTTGCTTGT 900
 QY 901 GGGTTTGTGTATTAATTAATTAATCTTCTATATATATATATATATATATATATATAT 960
 DB 901 GGGTTTGTGTATTAATTAATTAATCTTCTATATATATATATATATATATATATATAT 960
 QY 961 ATAAAAAATAAAAAATAAAAA 982
 DB 961 ATAAAAAATAAAAAATAAAAA 982

RESULT 2
 AAF85393
 ID AAF85393 standard; cDNA; 681 BP.
 XX
 AC AAF85393;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Nucleotide sequence of the floral homeotic protein PTD.
 XX
 KW Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
 KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KW fertility; sterility; ss.
 XX
 OS Populus balsamifera.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..681
 FT /*tag= a
 FT /product= "PTD"
 XX
 CA2319853-A1.
 XX
 PD 01-APR-2001.
 XX
 PF 02-OCT-2000; 2000CA-02319853.
 XX
 PR 01-OCT-1999; 99US-00410464.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
 XX
 DR WPI; 2001-336098/36.
 DR P-PSDB; AAB68435.
 XX

Novel isolated polynucleotide derived from Populus species, useful for
 producing transgenic plants having modified fertility characteristic,
 particularly sterility.

Claim 25; Page 42-43; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD.
 It is derived from Populus balsamifera subsp. trichocarpa. The
 specific location also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral
 homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 inflorescences on which floral primordia are developing. PTD is a
 homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are

CC	homologues of AGAMOUS (AG). The floral homeotic proteins and
CC	polynucleotides are useful for producing transgenic plants having
CC	modified fertility characteristics, particularly sterility
XX	
SQ	Sequence 681 BP; 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;
	Query Match 31.2%; Score 306.4; DB 4; Length 681;
	Best Local Similarity 70.1%; Pred. No. 1.2e-71;
	Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;
QY	1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCACAGGCAGGTGACC 60
DB	1 ATGGGTCGTGGNAAGTTGAANTCAGAAGATCGAAAACCCCACAACAGGCAGTCAAC 60
QY	61 TACTCCAAGAGAAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACGGTTCTTGAT 120
DB	61 TACTCGAAGAGAAGAAATGGTATTTCAGAAGAACCCCAAGACTCACTGTACTTTGTGAT 120
QY	121 GCCAAGGTCCTCATTTATGCTCTCCACACHTAATAAATGCACAGTATATCAGCCCT 180
DB	121 GCTAAGGTCCTCTTTATCATGTTCTCCAACACTAACAAACTCAATGAGTACATTAGCCCC 180
QY	181 ACCACTPACGACCAGAGTAGTGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240
DB	181 TCCACATCGACAAGAAGATCTACATCAATATCAGAACCTTTAGGCATAGATCTGTGG 240
QY	241 AGGACACACAGGAGTCGATGAAGAGACACCTTTGTGAAGTTGAAGAGATCAACAATAG 300
DB	241 GGCACTCAATACGAGAAAATGCAAGAGCACTTGAGGAAGCTGAATGATATCAATCATAG 300
QY	301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTTAATGGCTGAGCTTTGACGAG 360
DB	301 CTGAGACAAGAAATCAGGCAGAGGAGGAGGGCCCTGAATGATCTGAGCATTTGATCAT 360
QY	361 CTGGCTTCTCTTGACGATGAGTCAGTCGTCCTTTGGATGCCATAGCTCAAAGGAAGTAC 420
DB	361 CTGCGCGGCTTTGACACATATGACTGAAGCCTTGAATGGTGGTGGCAGGAATAC 420
QY	421 CATGTGATCAAAACTCAGACGGAGACCAACCAAGAAGAGTTTAAGAACTTTGAGGACAAAG 480
DB	421 CATGTGATCAAAACAACAAAACGMAACCTTACAGGAAGAAGGTGAAGAAATTTAGAGGAGA 480
QY	481 AGNGNMAATGCTGATGGCTATTTTTGACCAGGAAGCAGCCGGCGAGGATCCACAGTAT 540
DB	481 CATGGAAAGCCT-----CTTGATGGAATATGAAGCAAAACTAGAGGATCGACAGTAT 531
QY	541 GGTATTAGGACAATGAGGAGACTATCGAAATCTGCATTTGCATTTGTCAAATGGGCGAAT 600
DB	532 GGTTTAGTGGACAAT-----GAAGCTGCTGTTCACCTTCGAAATGGGCGTTC 579
QY	601 AACTGTGACATTTCCACTCCACCAACCCCTAACCTCCACCAC 642
DB	580 AACCTCTATGCAATCGGCTGATCAGCGGCACAACCAACCAAC 621

RESULT 3	
AAF85392	
ID	AAF85392 standard; cDNA; 946 BP.
XX	
XX	
AC	AAF85392;
XX	
XX	23-JUL-2001 (first entry)
DT	
XX	
DE	Nucleotide sequence of the floral homeotic protein PTD.
XX	
KW	Floral homeotic gene; PTD; PTLE; PTAG-1; PTAG-2; floral tissue; LEAFY;;
KX	LRF; FLORICALLA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
KW	fertility; sterility; ss.
XX	
OS	Populus balsamifera.
XX	
XX	
Key	Location/Qualifiers
FT	1..684
CDS	

FT		/ *tag= a	
FT		/ product= "PTD"	
XX			
XX			
XX	CAR2319853-A1.		
XX			
XX	01-APR-2001.		
XX			
XX			
XX	02-OCT-2000; 2000CA-02319853.		
XX			
XX	01-OCT-1999; 99US-00410464.		
XX			
XX	(UYOR-) UNIV OREGON HEALTH SCI.		
XX			
XX	Rottman WH, Straus SH, Brunner AM, Sheppard LA;		
XX			
XX	WPI; 2001-336098/36.		
DR	P-ZSD5; AAB68435.		
DR			
XX			
XX	Novel isolated polynucleotide derived from Populus species, useful for		
PT	producing transgenic plants having modified fertility characteristic,		
PT	particularly sterility.		
XX			
XX	Claim 25; Page 41-42; 69pp; English.		
PS			
XX			
CC	The present sequence encodes a floral homeotic protein, designated PTD.		
CC	It is derived from Populus balsamifera subsp. trichocarpa. The floral		
CC	specification also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral		
CC	homeotic proteins are expressed in floral tissues. PTLF is a homologue of		
CC	LEAFY (LFY) and FLORICAULA (FLC), and is expressed in immature		
CC	inflorescences on which floral primordia are developing. PTD is a		
CC	homologue of DEFICIENS (DBF), and is strongly expressed in stamen		
CC	primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are		
CC	homologues of AGAMOUS (AG). The floral homeotic proteins and		
CC	polynucleotides are useful for producing transgenic plants having		
CC	modified fertility characteristics, particularly sterility		
XX			
SQ	Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;		
XX			

Query Match	31.2%; Score 306.4; DB 4; Length 946;
Best Local Similarity	70.1%; Pred. No. 1.4e-71;
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;	
QY	1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACGACGACAGGTCAACC 60
DB	1 ATGGGTCTGTGNAAGATTGAAATCAAGAAGATCGAAACCCCAACACACGCAAGTCACC 60
QY	61 TACTCCAAAGAGAGAATAATGGGATCTTCAAGAAGCTCAGGAGCTCACCGTTCTCTGTGAT 120
DB	61 TACTCGAAGAGAGAATAATGGTATTTTCAGAAAGCCCAAGAAGTCATCTGTACTTTGTGAT 120
QY	121 GCCAAGGTCCTCCCTCAATTATGTCTCTCCAAACACTAATAAAATGACGAGTATATCAGCCCT 180
DB	121 GCTAAGGTCCTCTTATCATGTTCTCTCAACACATAACAACTCAATGAGTACATTAGCCCC 180
QY	181 ACCACTAGACCAAGAGATGTGTATGATGACTATCAGAAACATATGSSGATCGATCTGTGG 240
DB	181 TCCACATCGCAAGAAGAGACTCAGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240
QY	241 AGGACACACAGGAGTCCGATGAAGACACCTTTGGAAGTTTGAAGAGATCAACAATAAG 300
DB	241 GGCACTCAATACGAGAAATGCAAGAGCACTTTGAGGAAGCTGAATGATATCAATCATAA 300
QY	301 CTGAGGAGAGAGATCAGGCAGAGGTTTGGGCCATGATCTAAATGGCTTGAGCTTTGACGAG 360
DB	301 CTGAGACAAGAAATTCAGGCAGAGGAGGAGAGGGCCCTGAATGATCTGAGCATTTGATCAT 360
QY	361 CTGGCTTCTCTTTGACGATGAGATGCAGTCTTCTCTTGGATGCCATPACGTCAAAGGAAGTAC 420
DB	361 CTGCGCGGTCTTTGAGCAACATATGACTGAAGCCTTTGAATGGTGTGGCGGAGGAAGTAC 420
QY	421 CATGTGATCAAACTCAGACGGAGACCAACGAGAGAGGTTTAGRACCTTGGACCAAGA 480
DB	421 CATGTGATCAAAACACAAAACGAAACCTTACAGGAAGAGGTTGAAGATTTTAGAGAGAGA 480

QY 481 AGAGGAAACATGCTGCATGCTATTTTGACAGGAAGCAGCGCGGAGGATCCACAGTAT 540
 DB |||||
 QY 481 CATGGAACCT- - - - -CTTGATGGAATATGAGCAAACTAGAGGATCCACAGTAT 531
 DB |||||
 QY 541 GGTATAGGCAATAGAGGAGACTAGCAATCTCAGTTCGATTTGCAATGGGGGGAAT 600
 DB |||||
 QY 532 GGTATTAGTGACAAT- - - - -GAAGCTGCTGTTGCACTTGCATTTGCAATGGGGCTTCC 579
 DB |||||
 QY 601 AACTTTGACACTTTCCACCTCCACCCCTAACTCCACCAC 642
 DB |||||
 QY 580 AACCTTATGATTCGGCTGCATCAGGGCAACACCAC 621
 DB |||||

RESULT 4

ABK88485
 ID ABK88485 standard; cDNA; 946 BP.

AC ABK88485;

XX 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)

XX Poplar protein transduction domain, PTD, cDNA.

XX Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;
 KW protein transduction domain; floral homeotic gene;
 KW floral-specific expression; cytotoxin; fertility; sterility; PTLF;
 KW PTAG-1; PTAG-2.

XX Populus balsamifera; subsp. trichocarpa.

XX Key Location/Qualifiers
 FT CDS 1..684
 FT /*tag= a
 FT /product= "PTD"

XX US6395892-B1.

XX 28-MAY-2002.

XX 01-OCT-1999; 99US-00410464.

XX 06-APR-1998; 98US-0080851P.

XX 06-APR-1999; 99US-00287700.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Strauss SH, Rottmann W, Brunner A, Sheppard L;

XX WPI; 2002-572853/61.

XX P-PSDB; ABG30865.

XX New protein transduction domain promoter nucleic acid molecule useful for
 PT producing transgenic plants having modified fertility characteristics,
 PT particularly sterility.

XX Example 1; Col 35-38; 46pp; English.

XX The invention relates to an isolated nucleic acid molecule especially a
 CC protein transduction domain (PTD) promoter: (i) that hybridises under
 CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium
 CC dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
 CC and is the homologue of DEFICIENS. Also includes are a recombinant
 CC nucleic acid comprising the PTD promoter, a cell transformed with the
 CC recombinant nucleic acid and a transgenic plant comprising the
 CC transformed cell. The PTD promoter is useful to obtain floral-specific
 CC expression of genes such as cytotoxins, that are employed in genetic
 CC ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Genetic constructs comprising
 CC antisense versions or dominant negative mutants of PTD are useful in
 CC producing genetically engineered Poplars and other trees, and for sense

CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1 and
 CC PTAG-2 (none are defined). The present sequence is the PTD cDNA. (Updated
 CC on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 31.2%; Score 306.4; DB 6; Length 946;

Best Local Similarity 70.1%; Pred. No. 1.4e-71;

Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAAATCAAGCTGATCGAAACACGACCAACAGCAGCGGTGACC 60

DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAAACAGCAAGTCAACC 60

QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAAAGCTCAGGAGCTCAGCGTTCTCTGTGAT 120

DB 61 TACTCGAAGAGAGAAATGGTATTTTCAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 120

QY 121 GCCAAGTCTCCCTCATATATGCTCTCCAACTATAATAATGCACAGATATATCAGCCCT 180

DB 121 GCTAAGTCTCTCTTATCATGTTCTCCAACTAACCAACTCAATGAGTACATTTAGCCCC 180

QY 181 ACCACTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

DB 181 TCCATCATGCAAGAGAGATCTAGATCAATATCAGAACGCTTTAGGATAGATCTGTGG 240

QY 241 AGGACACACGAGGAGTGCATGAAAGACACCTTTGTGAAAGTTGAAAGAGATCAACAATAAG 300

DB 241 GGCATCAATACGAGAAATGCAAGAGCCTTTGAGGAAGCTGATGATATCAATCAATAAG 300

QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTAAATGCCCTGAGTTTGCAGAG 360

DB 301 CTGAGACAAAGAAATCAGGACAGGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360

QY 361 CTGGCTTCTCTTGACGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

DB 361 CTGGCGGCTCTTGAGCAACATATGATGAAAGCTTGAATGTTGTTGCGTGGCAGGAGTAC 420

QY 421 CATGTGATCAAACTCAGACGGAGACCAACAGAGAGGTTAGAACTTTGGAGCAAGA 480

DB 421 CATGTGATCAAAACACAAACCAACCTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480

QY 481 AGAGAAACATGCTGCTGCTGCTATTTTGACAGGAAGCAGCGCGGAGGATCCACAGTAT 540

DB 481 CATGGAACCT- - - - -CTTGATGGAATATGAGCAAACTAGAGGATCCACAGTAT 531

QY 541 GGTATAGGACAATGAGGAGAGACTACGAATCTGCACTTGCATTTGCAATGGGGGGAAT 600

DB 532 GGTATTAGTGACAAT- - - - -GAAGCTGCTGTTGCACTTGCATTTGCAATGGGGCTTCC 579

QY 601 AACTTTGACACTTTCCACCTCCACCCCTTAACCTCCACCAC 642

DB 580 AACCTTATGATTCGGCTGCATCAGGGCAACACCAC 621

RESULT 5

ACA62518

ID ACA62518 standard; cDNA; 946 BP.

XX ACA62518;

XX 18-AUG-2003 (first entry)

XX Poplar homeotic gene PTD, cDNA.

XX Poplar; ss; gene; PTD; deficient; homeotic gene; floral development;
 KW sterile tree; pulp; paper; plant.

XX Populus balsamifera subsp. trichocarpa.

XX Key Location/Qualifiers

FT CDS 1..684

FT /*tag= a

FT	/product= "PTD"
FT	/note= "This CDS is specifically claimed in claim 1"
XX	
PN	US2003033628-A1.
XX	
PD	13-FEB-2003.
XX	
PD	21-MAR-2002; 2002US-00104580.
XX	
PR	06-APR-1998; 98US-0080851P.
XX	
PR	06-APR-1999; 99US-00287700.
PR	01-OCT-1999; 99US-00410454..
XX	
PA	(UYOR-) UNIV OREGON HEALTH SCI.
XX	
FI	Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX	
DR	WPI; 2003-4566273/44.
DR	P-PSDB; ABU61893.
XX	
PT	New floral homeotic nucleic acid molecules, useful for the manipulation
PT	of flowering in Poplar and other plant species, and for producing
PT	transgenic plants having modified fertility characteristics, particularly
PT	sterility.
XX	
PS	Claim 1; Page 20-21; 48pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule comprising at
CC	least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
CC	4 homeotic genes from poplar, PTIF (LEAFY and FLORICA homologues), PTD
CC	(DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).
CC	Also included are a recombinant nucleic acid molecule comprising a
CC	promoter sequence operably linked to the nucleic acid molecule, a cell
CC	transformed with the nucleic acid molecule, a transgenic plant comprising
CC	the recombinant nucleic acid molecule and the purified proteins encoded
CC	by the nucleic acids. The nucleic acid molecules are useful for the
CC	manipulation of flowering in Poplar and other plant species, for
CC	producing transgenic plants having modified fertility characteristics
CC	(particularly sterility) and in the pulp and paper industries. The
CC	present sequence is the poplar PTD cDNA
XX	
SO	Sequence 946 BP: 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match	31.2%	Score 306.4;	DB 8;	Length 946;
Best Local Similarity	70.1%;	Pred. No. 1.4e-71;		
Matches 450;	Conservative 0;	Mismatches 171;	Indels 21;	Gaps 2;
Qy	1	ATGCGCGGGAGAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCAGGTGACC	60	
Db	1	ATGGGTCTGTGGAAAGATTGAATCAAGAAGATCGAAAACCCCACAAACAGGCAAGTCACC	60	
Qy	61	TACTCCAAGAGAGAAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT	120	
Db	61	TACTCGAAGAGAGAAGAAATGGTATTTTCAAGAAGCCCAAGAACTCATCTGTACTTTGTGAT	120	
Qy	121	GCCAAAGGTCTCCCTCATTATCTCTCCAAACACTAATAAAATGCACGAGTATATCAGGCCCT	180	
Db	121	GCTAAGGTCTCTTTATCATGTTCTCCAAACACTAACAACTCAATGAGTACATTAGCCCC	180	
Qy	181	ACCACTACGACCAAGAGTATGTTATGATGACTATCAGAAAACTATGCGGATCGATCTGTGG	240	
Db	181	TCCACATCGACAAAAGAGATCTACGATCAATATCAGAACCGTTTAGGCATAGATCTGTGG	240	
Qy	241	AGGACACACGAGGAGTCCGATGAAGACACCTTTGTGGAGTTGAAGAGATCAACAATAAG	300	
Db	241	GGCACTCAATACGAGAAATCAAGAGGCACTTTGGAGGACTTGAATGATATCAATCAATAAG	300	
Qy	301	CTGAGGAGAGAGATCAGGCAGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAG	360	
Db	301	CTGAGACAAAGAAATCAGGCAGAGGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT	360	
Qy	361	CTGGCTTCTCTTGACGATGACATGCAGTCTTCTTGGATGCCATACGTCAAAGGAAGTAC	420	

Db	361	CTGCGGGTCTTTGAGCAACATATGACTGAAGCCTTTGTAATGGTGTGCGTGCGGAGGAATGAC	420
Qy	421	CATGTGATCAAAACCTCAGACGGAGACCAACCAAGAAGGCTTAAGAACTTTGGAGCAAGA	480
Db	421	CATGTGATCAAAACACAAACGAAACCTTACAGGAAGAAGGTGAAGAAATTTTAGAGGAGAGA	480
Qy	481	AGAGGAACATGCTGCATGGCTATTTTTCACAGGAACAGCCGGCGAGGATCCACAGTAT	540
Db	481	CATGGAACCT-----CTTGATGGAATATGAAGCAAAACTAGAGGATCGACAGTAT	531
Qy	541	GGTTATGAGCAACATGAGGGAGACTAGCAATCTGCACCTTGCATTTGTCAAATGGGGCGAAT	600
Db	532	GGTTTAGTGACAAAT-----GAGCTGCTGTGCACTTGCAATGGGGCTTCC	579
Qy	601	AACCTGTACATTTTCCACTCCACACCCCTAACCTCCACAC	642
Db	580	AACCTCTATGCAATTCGGCTCTCATCAGGGCACAACCAACAC	621

RESULT 6	
AAZ57943	standard; cdna; 924 BP.
XX	
XX	
XX	AAZ57943;
XX	AC
XX	11-APR-2000 (first entry)
DT	
DT	
XX	Poplar floral homeotic gene PTD cdna.
DE	
XX	
XX	Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
KW	fertility; ss.
KW	
XX	Populus balsamifera subsp. trichocarpa.
OS	
XX	
XX	Key
FH	Location/Qualifiers
FT	1. .684
CDS	/*tag= a
FT	/note= "the coding region is also specifically claimed in
FT	Claim 1"
FT	
FT	

CA2227940-Al.
05-OCT-1999.
07-APR-1998; 98CA-0227940.
06-APR-1998; 98US-00080851.
(UYOR-) UNIV OREGON HEALTH SCI.
Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
WPI; 2000-106662/10.
P-PSDB; AAY58654.
Nucleic acid from *Populus trichocarpa* genes, useful for producing transgenic plants, particularly trees, with modified fertility characteristics such as sterility.
Claim 1; Page 46-47; 92pp; English.
The present sequence is that of cDNA encoding *Populus balsamifera* subsp. *trichocarpa* PTD protein (see AAY58654). The PTD gene (see AAZ57942) is 1 of 4 newly identified floral homeotic genes from this poplar species. It is a homologue of *DEPICIENS* and is expressed strongly in stamen primordia from the onset of organogenesis, and is also expressed at low levels in carpel primordia. The invention provides nucleic acid sequences of these 4 *Populus* genes, the corresponding cDNA sequences (see AAZ57942-49) and deduced amino acid sequences (see AAY58454-57). It also provides methods of using the gene and cDNA sequences to produce genetically engineered *Populus* species and other trees having modified fertility characteristics, including sterility. Genetic constructs useful in producing genetically engineered *Populus* and other trees include

CC antisense versions of PTD, dominant negative mutants, and constructs
 CC useful for sense suppression. Promoter sequences may be used to obtain
 CC floral specific expression of genes such as cytotoxins that may be used
 CC in genetic ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Sterile trees allow increased wood
 CC yield and a reduction in the production of allergens such as pollen
 XX
 SQ Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Query Match 30.9%; Score 303.2; DB 3; Length 924;
 Best Local Similarity 69.8%; Pred. No. 9.7e-71;
 Matches 448; Conservative 0; Mismatches 173; Indels 21; Gaps 2;

QY 1 ATGCGCGCGGAGATGAAATCAAGCTGATCGAAACCCAGACCAACGCGAGGTGACC 60
 DB |||||
 QY 1 ATGCGTCTGGAAGATTGAAATCAAGAGATCGAAACCCCAACACGCGCAAGTCACC 60
 DB |||||
 QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGCTCACCGTCTCTCTGAT 120
 DB |||||
 QY 61 TACTCGAAGAGAAATGGTATTTTCAGAAAGCCCAAGACTCACTGACTTTGTGAT 120
 DB |||||
 QY 121 GCCAAGGTCTCCCTCATTTGCTCTCCAAACACTAATAAAATGCACGAGTATATCAGCCCT 180
 DB |||||
 QY 121 GCTAAGGTCTCTTATCATTTGCTCCCAACACTAAACAACCTCAATGAGTACATTAGCCCC 180
 DB |||||
 QY 181 ACCACTAGCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB |||||
 QY 181 TCCACATCGCAAGAGAGATCTAGATCAATATCAGAAACGCTTTAGGCATAGATCTGTG 240
 DB |||||
 QY 241 AGGACACACAGAGAGTGCATGAAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAAG 300
 DB |||||
 QY 241 GGCACTCAATACGAGAAATGCAAGACACTTGAGGAGCTGATGATATCATCATAG 300
 DB |||||
 QY 301 CTGAGGAGAGATCAGCGAGAGTTGGGCCATGATCTAAATGCGCTGAGCTTTGACGAG 360
 DB |||||
 QY 301 CTGAGACAAGAAATCAGCGAGAGAGAGAGAGGCGCTGATGATGATGATGATGATGAT 360
 DB |||||
 QY 361 CTGGCTTCTCTTGACGATGAGATGAGTCTTCTTGGATGCCATACGTCAAGGAAGTAC 420
 DB |||||
 QY 361 CTGGCGGTCTTGACCAACATATGACTGAAGCTTTGATGCTGCTGGCAGGAAGTAC 420
 DB |||||
 QY 421 CATGTATCAAACTCAGACGAGACACCAAGAGAGGTTAAGAACTTGGAGCAAGA 480
 DB |||||
 QY 421 CATGTATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480
 DB |||||
 QY 481 AGAGGAACATGCTGCATGCTATTTTGACGAGAGACCGCGGAGGATCCACAGTAT 540
 DB |||||
 QY 481 CATGGAACCT-----CTTGATGGAATATGAAGCAAACTAGAGGATGACAGTAT 531
 DB |||||
 QY 541 GGTATGAGGACATGAGGAGACTAGCAATCTGCACCTTGCATTTGCAATGTCAAATGGGCGAAT 600
 DB |||||
 QY 532 GGTATTAGTGACAAAT-----GAAGTGTCTGTTGCACTTGCATTTCAAATGGGCTTCC 579
 DB |||||
 QY 601 AACTGTGACTTTCACCTCCACCCCTCAACCTCAACCCAC 642
 DB |||||
 QY 580 AACCTCTATGATTCGCGCTGCATCATCGGCGCAACACCCAC 621
 DB |||||

RESULT 7

AAC55879

ID AAC55879 standard; DNA; 999 BP.

XX AC

XX AC AAC55879;

XX XX

DT 25-JAN-2001 (first entry)

XX DE

XX Eucalyptus grandis transcription factor DNA sequence #10.

XX XX

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;

XX basic helix-loop-helix zipper; homeotic; homeodomain; MADS;

XX homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;

XX type 2 Cys2His2; CCAAT box element; MYB; ss.

XX Eucalyptus grandis.
 OS
 XX WO200053724-A2.
 PN
 XX 14-SEP-2000.
 PD
 XX 09-MAR-2000; 2000WO-US006112.
 PF
 XX 11-MAR-1999; 99US-00266513.
 PR
 XX 18-AUG-1999; 99US-0149485P.
 XX
 (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 XX
 PI Wood M, McGrath A, Shenk MA, Glenn M;
 DR WPI; 2000-579369/54.
 XX
 XX New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide.
 XX
 XX Claim 1; Page 46-47; 747pp; English.
 XX
 CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
 CC sequence for one such transcription factor. The transcription factor may
 CC be used to produce a plant having modified gene expression such as a
 CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
 CC mahogany species or to modify the activity of a polypeptide in a plant.
 CC The transcription factors of the present invention are members from the
 CC following families of regulatory proteins: bZIP, bZIP family of G-box
 CC binding factors, basic helix-loop-helix zipper,
 CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
 CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and
 CC MYB
 XX
 SQ Sequence 989 BP; 292 A; 233 C; 262 G; 202 T; 0 U; 0 Other;

Query Match 25.2%; Score 247.2; DB 3; Length 989;
 Best Local Similarity 64.5%; Pred. No. 9.8e-56;
 Matches 388; Conservative 0; Mismatches 208; Indels 6; Gaps 1;

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 QY 7 ATGCGGAGGGGAAGATCCAGATCAAGCTGATGAGAACACGACGACCGGAGGTGACC 66
 DB |||||
 QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAACGTTCTCTGTGAT 120
 DB |||||
 QY 67 TACTCGAAGCAGCAGGAGGCTCTTCAAGAGGCGAAGCTCAGGCTCAGGCTCCTAGGCGAC 126
 DB |||||
 QY 121 GCCAAGGTCTCCCTCATTTGCTCTCCAAACACTAATAAAATGCACGAGTATATCAGCCCT 180
 DB |||||
 QY 127 CCCAAGGTCTCCATCATCATGATCTCCAGCAGCGGCAAGCTCCACGAGTACATCAGCCCC 186
 DB |||||
 QY 181 ACCACTAGCAGCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB |||||
 QY 187 TCCACCTCAACGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 246
 DB |||||
 QY 241 AGGACACACGAGAGTGCATGAAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAAG 300
 DB |||||
 QY 247 AGCTCTCATGATGAGAGATGCAAGAGAACCTGAGGAAGCTGAGGAGGTGAACAAGAG 306
 DB |||||
 QY 301 CTGAGGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360
 DB |||||
 QY 307 CTTGAGCTGGAGGTTCAGGAGGAGGTTTCGGGAAGGACTGAATGATGATGATGATGATG 366
 DB |||||
 QY 361 CTGGCTTCTCTTGACGATGAGATGCACTCTTCTTGGATGCCATACGTCAAGGAAGTAC 420
 DB |||||
 QY 367 TTGTGCGGTCTTGAGCAAGATATGACAAACGCGCTTAGCTGATCCGTGAACGGAAGTAC 426
 DB |||||
 QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTAAGAACTTTAGAGGAGAGA 480
 DB |||||


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PN WO9321322-A1.
PD 28-OCT-1993.
PF 13-APR-1993; 93WO-US003508.
XX 13-APR-1992; 92US-00867580.
PR 06-JUL-1992; 92US-00909589.
XX (UVRQ ) UNIV ROCKEFELLER.
XX Halfter U, Van Der Krol AR, Kush A, Chua N;
DR WPI; 1993-351732/44.
DR P-PSDB; AAR43385.
XX
PT Plant organ morphogenesis control and determ. - by regulating the
PT expression of homeotic genes which determine the identity of the organ.
XX
PS Claim 13; Fig 2; 74pp; English.
XX
CC The homeotic gene green petal from petunia has been cloned and
CC characterised previously. The gene was used in a new method for
CC controlling the morphogenesis of plant organs comprising regulating the
CC expression of the gene using ectopic expression. Such a method can be
CC used to determine and control plant organ morphogenesis, such as
CC modifying petals without altering the reproductive portions of the
CC flower. See also AQA51190-1. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 882 BP; 306 A; 155 C; 182 G; 239 T; 0 U; 0 Other;

Query Match 24.18; Score 236.4; DB 2; Length 882;
Best Local Similarity 62.08; Pred. No. 7.3e-53;
Matches 397; Conservative 0; Mismatches 231; Indels 12; Gaps 1;

Qy 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCAACAGACCAACAGGCGAGTGACC 60
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Qy 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 120
Db 78 TATTCTAAGAGAGAAATGGACTTTTCAAGAGGCTTAATGAATCACTGCTTCTTTGTGAT 137
Qy 121 GCCAAGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180
Db 138 GCCAAGTTTCCATAATTATGATTTCCAGTACTGGCAGCTTCATGAATTCATTAGTCCA 197
Qy 181 ACNCTACGACCAAGAGATGTATGATGACTATCAGAAACTATGGGATCGATCTGTGG 240
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Db 258 AACTCCACTATGNAATGCAAGGCACTGAGAGAGCTAAGGAAGTAAATAGGAT 317
Qy 301 CTGAGGAGAGATCAGGCAAGAGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360
Db 318 CTCGAAAGAGATCAGGCAAGAGTGGGAGAAAGCCTAAACGATCTGAATATGAGCAG 377
Qy 361 CTGCTCTCTCTGACGATGATGATGCTTCTTCTGATGCCATCTCAAGAGGAGTAC 420
Db 378 TTGAGAGAGCTCATGNAATGTGCAATTTCTCAAGCTTATCTGTAAGAAAGTAT 437
Qy 421 CATGTGATCAAACTCAGACGAGACCAACAGAGAGGTTAAGAACTTGGAGCAAGA 480
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Qy 481 AGAGGAACATGCTGATGCTATTTTGACCAGAGAGCGCGGAGGATCCACAGTAT 540
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Qy 541 GGTATGAGCAATGAGGGAGACTACGAATCTGCACTTGTGCTTGTCAATGTGGAATGGGCGAAT 600
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Qy 601 AACTTGTACACTTTCCACCTCCACCAACCTAACCTCCACC 640
Db 606 CGCATATTAGCTTACGCTTCAACCAACCAACCAACCCAGC 645

RESULT 10
AAC51525
ID AAC51525 standard; DNA; 954 BP.
XX
AC AAC51525;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68842.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
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Query Match 23.2%; Score 227.4; DB 3; Length 954;
Best Local Similarity 61.0%; Pred. No. 1.9e-50;
Matches 391; Conservative 0; Mismatches 241; Indels 9; Gaps 1;

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DB 29 ATGGCGAGAGGAGATCCAGATCAAGAGATAGAGACCAACAGACAGCAAGTGAGC 88

RESULT 12
AAC51790
ID AAC51790 standard; DNA; 1170 BP.
XX
AC AAC51790;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69758.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150586P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 23.08; Score 225.8; DB 3; Length 1170;
Best Local Similarity 60.8; Pred. No. 5.7e-50;
Matches 390; Conservative 0; Mismatches 242; Indels 9; Gaps 1;

QY 1 ATGGCGCGCGGAAGATTGAATCAAGCTGATCGAAACAGACCAACAGCGAGGTGACC 60
DB 253 ATGGCAGAGGAGATCCAGATCAAGAGTAGAGNACCAGACAAACAGCAAGTGACG 312
QY 61 TACTCAAGAGAGAAATGGGAATCTCAAGAGCTCAGAGCTCCGGTTCTCTGTGAT 120
DB 313 TATTCAAGAGAGAAATGGTTATTCAAGAAAGCACATGAGCTCAGCGTTTGTGTGAT 372
QY 121 GCCAAGTCTCCCTCATTATGCTCTCCACACTAATAAATGACAGGTATATCAGCCCT 180
DB 373 GCTAGGGTTTCGATTATCAATGTTCTCTAGTCCCAACAGCTTCATGATATATCAGCCCT 432
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QY 181 ACCACTAGACCAAGAGTAGTATGATGACTATCAGAAAACCTATGGGATCGATCTGG 240
DB 433 AACACCAACAGAGAGATCGTAGATCTGTAACAACTATTCTGATGTCGATTTGG 492
QY 241 AGGACACAGGAGAGTCGATGAAGACACCTTTGTGGAAGTTGAAAGAGATCAACAATAG 300
DB 493 GCCACTCAATATGAGCGAATGCAAGAAACCAAGAGGAACTGTTGGAGACAAATAGAAAT 552
QY 301 CTGAGGAGAGATCAGCAGAGGTTGGCCCATGATCTAAATGGGCTGAGCTTTCAGCAG 360
DB 553 CTCGGAGCTCAGATCAAGCAGAGGCTAGGTAGTGTTTGGACAACTTGACATTCAGGAG 612
QY 361 CTGGCTTCTCTTGACCATGAGATGCAGTCTTCTTTGGATGCCATACGTCAGAGGAGTAC 420
DB 613 CTGGCTGCTTTGAGGATGAATGGAACAACCTTTCAAACTCGTTCGGAGCGCAAGTTC 672
QY 421 CATGTGATCAAAACTCAGACGGAGACCAACCAAGAGAAGTTAAGAACTTGGAGCAAGA 480
DB 673 AAATCTCTTTGGGATCAGATCGAGACCAACCAAGAAAAAGAACAAAGTCAACAGACATA 732
QY 481 AGAGGAACATCTGCTGATGGCTATTTTGACAGGAAGCAGCGCGGAGGATCCACAGTAT 540
DB 733 CAAAGATCTCATACA-----TGAGCTGGAACTAAGAGCTGAAGATCCTCATTAT 783
QY 541 GGTATGAGGACAATGAGGAGACTACGAATCTGCATTTGCATTTGCAATGGGGCGAAT 600
DB 784 GGACTAGTAGACATGAGGAGATTACGACTCAGTTCTTTGGATACCAAAATCGAGGGTCA 843
QY 601 AACTTGTACATTTCCACTCCACCACCCCTAACCTCCACCA 641
DB 844 CGTGTTCAGCTCTCTGTTTCCACCAGAACCATCACCATA 884

RESULT 13
AAC40685
ID AAC40685 standard; DNA; 954 BP.
XX
AC AAC40685;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29191.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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Db 311 GGAACCGACATCAAGACCATCTTTGACCGGTACCAGCAGGCCATCGGACCAGCCTATGG 370
 Qy 241 AGGACACACAGAGAGTGCATGAAGACACCTTGTGGAAGTTGAAGAGATCAACATTAAG 300
 Db 371 ATCAGCAGTATGAGAATATGACGCGCACCTGAGCCATCTCAAGGACATCAATCGTGT 430
 Qy 301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTAAATGGCTGAGCTTTGACGAG 360
 Db 431 CTGCGCACAGATTAGGCAAGATGGGCGAGATCTGGACAGTCTGGACCTTCGACGAG 490
 Qy 361 CTGCTTCTCTTACGAGATGATGCGATCTTCCTTGGATGCCATAGCTCAAGGGAAGTAC 420
 Db 491 CTGCGCGCTCTCAGCAAAAACGTCGACGCGCTCTCAAGGAGGTTCCGCATAGGAAGTAC 550
 Qy 421 CATGTGATCAAACTCAGCGGAGACACACAGAAGAGTTAAGAACTTGGAGCAAGCA 480
 Db 551 CATGTGATCAGCGGAGACTGATACCTCAAGAAAAGGTGAAGCACTCGACAGGCG 610
 Qy 481 AGAGGAAACATGCTGCATG 499
 Db 611 TACAAGAACCTCGACGAGG 629

RESULT 15

AAC56790

ID AAC56790 standard; DNA; 409 BP.

XX AC AAC56790;

XX

DT 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor DNA sequence #661.

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XX

CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and
 CC MYB
 XX
 SQ Sequence 409 BP; 133 A; 96 C; 105 G; 75 T; 0 U; 0 Other;
 Query Match 19.7%; Score 193; DB 3; Length 409;
 Best Local Similarity 72.5%; Pred. No. 2.2e-41;
 Matches 250; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
 Qy 19 GAAATCAAGCTGATCGAAAACCCAGACCAACAGCAGCTGACCTACTCCAGAGAGAGAAAT 78
 Db 1 GAGAGACAGAAATTAGAACGACACAGCAGGCAAGTGACCTACTCGAAGCGGAGGAAT 60
 Qy 79 GGGATCTTCAAGAAAGGCTCAGGAGCTCACCGTTCTCTGTGATGCCAAGGTCTCCCTCAT 138
 Db 61 GGCATCTTCAAGAAAGCCACGAGCTCACCGTCTCTGCGACGCTAGGGTTTCCATCTC 120
 Qy 139 ATGCTCTCCACACTAATAAATGACAGAGTATATCAGCCCTACCTACCTAGCAGCAGAGT 198
 Db 121 ATGCTCTCCGCAACAAGAGCTCCACGAGTACATCAGCCCCCACCACGACACAAAAGG 180
 Qy 199 ATGTATGATGACTATCAGAAAACCTATGGGATCGATCTGTGGAGGACACACAGGAGTCTG 258
 Db 181 ATGATTGATGATTACCAAGAGGCTCTTGGGATCGATCTGTGGACTACACACTACGATAGA 240
 Qy 259 ATGAAAGACACCTTGTGGAAGTTGAAAGAGATCAACAATAAGCTGAGGAGAGAGATCAGG 318
 Db 241 ATGCAAGAGGAGTTGAGGAACTGAGGAGGTTAATAACAATTTTCGGAAGAGAAATAAGG 300
 Qy 319 CAGAGGTTGGGCCATGATCTAAATGGCCTTGAGCTTTGACGAGCTG 363
 Db 301 CAGATATTGGGCCACGATTTGAACAGAGCTGAGCTACGAGAACTG 345

Search completed: September 25, 2004, 16:09:52

Job time : 457.966 secs

Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
 type 2 Cys2His2; CCAAT box element; MYB; ss.
 Eucalyptus grandis.

WO200053724-A2.

14-SEP-2000.

09-MAR-2000; 2000WO-US006112.

11-MAR-1999; 99US-00266513.

18-AUG-1999; 99US-0149485P.

(GENE-) GENESIS RES & DEV CORP LTD.
 (FLET-) FLETCHER CHALLENGE FORESTS LTD.

Wood M, McGrath A, Shenk MA, Glenn M;

WPI; 2000-579369/54.

New isolated polynucleotide encoding a plant transcription factor for
 producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 having modified gene expression or modified activity of a polypeptide.

Claim 1; Page 515; 747pp; English.

The present invention relates to novel plant transcription factors from
 Eucalyptus grandis or Pinus radiata. The present sequence is the coding
 sequence for one such transcription factor. The transcription factor may
 be used to produce a plant having modified gene expression such as a
 woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
 mahogany species or to modify the activity of a polypeptide in a plant.
 The transcription factors of the present invention are members from the
 following families of regulatory proteins: bZIP, bZIP family of G-box
 binding factors, basic helix-loop-helix zipper, LIM domain, AP2
 homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 14:17:32 ; Search time 4147.76 Seconds
(without alignments)
10261.660 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcgggggaattgta.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rnd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	953.4	97.1	1102	8	MDO251116	AJ251116 Malus dom
2	633.8	64.5	1043	8	AB081093	AB081093 Malus x d
3	452.8	46.1	473	8	AB081094	AB081094 Malus x d
4	391.4	39.9	1014	8	AB055966	AB055966 Rosa rugo
5	306.4	31.2	681	6	AR372459	AR372459 Sequence
6	306.4	31.2	946	6	AR372458	AR372458 Sequence
7	297.4	30.3	906	8	GHY9724	AJ009724 Gerbera h
8	282.8	28.8	998	8	AMDEPI	X52023 A majus def
9	276.8	28.2	994	8	AF230704	AF230704 Petunia x
10	276.6	28.2	895	8	LEIDR6	X60759 L. esculentu
11	275.2	28.0	939	8	AF230703	AF230703 Hydrangea
12	273.4	27.8	945	8	AY098734	AY098734 Lycopersi
13	254.6	25.9	924	8	STPD4	X67508 S. tuberosum
14	248.6	25.3	1005	8	AB071378	AB071378 Lilium re
15	244	24.8	1039	8	AF503313	AF503313 Lilium lo
16	239.6	24.4	965	8	ALFMBP	L41727 Medicago sa
17	237	24.1	926	6	AX478039	AX478039 Sequence
18	236.4	24.1	881	8	PHGP	X69946 P. hybrida m
19	235.2	24.0	952	8	AB094964	AB094964 Asparagus
20	234.2	23.8	1113	8	NTMADSBOX	X96428 N. tabacum m
21	228	23.2	1002	8	AB094965	AB094965 Tulipa ge
22	227.4	23.2	730	8	AY142590	AY142590 Arabidops
23	227.4	23.2	959	8	AY087369	AY087369 Arabidops
24	227.4	23.2	960	8	AY070397	AY070397 Arabidops
25	226.2	23.0	763	8	AY162881	AY162881 Platanus
26	225.8	23.0	1010	8	ATHAPETELA	M86357 A. thaliana
27	225.8	23.0	1084	8	AB003323	AB003323 Oryza sat
28	225.8	23.0	1210	8	AK069317	AK069317 Oryza sat
29	225.2	22.9	791	8	AB090869	AB090869 Silene co
30	224.2	22.8	1061	8	AF077760	AF077760 Oryza sat
31	222.2	22.6	959	8	AB007506	AB007506 Triticum
32	221.4	22.5	830	8	AY397762	AY397762 Chloranth
33	220.6	22.5	1129	8	AB099875	AB099875 Rosa rugo
34	220.2	22.4	920	8	BCU67455	U67455 Brassica ol
35	219.6	22.4	887	8	DCA271149	AJ271149 Daucus ca
36	219.6	22.4	941	8	AF124814	AF124814 Brassica
37	218.6	22.3	675	8	AY131391	AY131391 Brassica
38	218.4	22.2	844	8	AY173070	AY173070 Helianthu
39	218.2	22.2	852	8	AB050649	AB050649 Magnolia
40	217.4	22.1	1004	8	AF181479	AF181479 Zea mays
41	217.4	22.1	1257	6	AX478035	AX478035 Sequence
42	217.2	22.1	833	8	AF209729	AF209729 Hemerocal
43	216.8	22.1	1016	8	AB094966	AB094966 Tulipa ge
44	216.6	22.1	762	8	AY162882	AY162882 Platanus
45	215.6	22.0	793	8	AB090867	AB090867 Silene di

ALIGNMENTS

RESULT 1
MDO251116

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

MDO251116 1102 bp mRNA linear PLN 16-NOV-2001
Malus domestica mRNA for B-type MADS box protein (mads13 gene).
AJ251116
AJ251116.1 GI:16973293
B-type MADS box protein; mads13 gene.
Malus x domestica (apple tree)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

Pred. No. is the number of results predicted by chance to have a

REIRQRGLHDLNGLSYDRLSLDKQSSLDIAIRERKHYHVIKTQTETTKKKVKNLEER
RGNMLHGYEAAENPOCYVDNEGYDESALVLANGANNLYTFQLHNSDQLHHPNLH
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ORIGIN

Query Match 64.5%; Score 633.8; DB 8; Length 1043;
Best Local Similarity 85.3%; Pred. No. 2.8e-160;
Matches 794; Conservative 0; Mismatches 67; Indels 70; Gaps 5;
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DB 63 ATGGGTGCTGGAAGATTGATCAAGCTGATCGAAACACAGACCACAGCGAGGTGACC 122
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGCTCAGGAGCTCAGCGTTCTCTGTGAT 120
DB 123 TACTCCAGAGAGAAATGGGATCTTCAAGAAGCTCAGGAGCTCAGCGTTCTCTGTGAT 182
QY 121 GCCAAGTCTCCCTCATATGCTCTCCACACACTAATAAATGACAGGATATACAGCCCT 180
DB 183 GCCAAGTCTCCCTCATATGCTCTCCACACACTAATAAATGACAGGATATACAGCCCT 242
QY 181 ACCACTACGACCAAGATGATGATGACTATCAGAAACTATGGGGATCGATCTGTGG 240
DB 243 ACCACTACGACCAAGATGATGATGACTATCAGAAACTATGGGGATCGATCTGTGG 302
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DB 303 AGGACACACTACGAGTCTATGAAGACACCTTGTGGAGTGTGAAGATCAACAATAG 362
QY 301 CTGAGGAGAGATCAGCAGAGGTGGGCAATGATCTAAATGGCCCTGAGCTTTGACGAG 360
DB 363 CTGAGGAGAGATCAGCAGAGGTGGGCAATGATCTAAATGGCTGACGATGACGAT 422
QY 361 CTGCGCTCTCTGACGATGATGATGCTCTTCTTGGATGCCATACGTCGAAAGAGTAC 420
DB 423 CTGCGCTCTCTGACGATGATGATGCTCTTCTTGGATGCCATACGTCGAAAGAGTAC 482
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DB 543 AGAGGAAACATGCTGCATGCTATTTTGACAGAGAGCAGCGGAGGATCCACAGTAT 593
QY 541 GGTATGAGGACATGAGGAGATGACGATCTGCACTTGCATGTCATGTCAAATGGGCAAT 600
DB 594 TGTTATGTGGCAATGAGGAGAGATGATGAATCTGCACTTGTGTGGCAATGGGCAAT 653
QY 601 AACTTGTACACTTT-----CCACCTCCACACCCCTAACCT---C 636
DB 654 AACTTGTACACTTTCCAGCTCCACCGCAACTCCGACAGCTCCACACCCCTAACCTCCAC 713
QY 637 CACACGAGAGAGCTCGCTCGGCTCCTCCATCTACTCATCTGACGATCTCCGCTTGTCT 696
DB 714 CACACAGAGAGAGTCTCGCTCGGCTCCTCCATCTACTCATCTGACGATCTCCGCTTGTCT 773
QY 697 TGATCGTGATCTGAGATGATTAATCATCACTAAGTTATATATTAAGGTCACCTTA--- 752
DB 774 TGATCGTGATCCGAGAGATGATTAATGCCACTAAGTTATATTAAGGTCACCTTAAT 833
QY 753 -----TAAGTCTTTTGTCTAAAGTTTGTCTTGGTACTA 789
DB 834 TTTATATATATTCCTCAGAGACTTAACTGCTTATGTTCTAAAGTGTCTTTTAACTGATGA 893
QY 790 TCTTTAGCAGAGGATGATGATGCTGCTGCTGAAACAGATGCAATAATATGTTGT 849
DB 894 TCTTTAGGCT-----ACTTGATTTACCTCTAAACACATATGCAATAATATCTGG 943
QY 850 GGTGTTTTTAATCAATGATGACACTAAAAAA 880
DB 944 GATGTTTTTATGATTAACACTAACACAA 974

RESULT 3

AB081094
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Malus x domestica (apple tree)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.
1
Matsumoto,S., Ohtsubo,T. and Soejima,J.
Cloning and sequencing of apple MADS-box genes 'MdPI1', 'MdTM6' and
'MdMADS13',
Unpublished
2 (bases 1 to 473)
Ohtsubo,T. and Matsumoto,S.
Direct Submission
Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,
Gifu 501-1193, Japan (E-mail:shmatsum@gifu-u.ac.jp,
Tel:81-58-293-2257, Fax:81-58-293-2207)
1..473
Location/Qualifiers
/organism="Malus x domestica"
/mol_type="mRNA"
/cultivar="Indo"
/db_xref="taxon:3750"
/tissue_type="young floral parts"
1..473
/gene="MdMADS13"
/cds_start=2
/product="MADS-box protein"
/protein_id="BAC11908.1"
/db_xref="GI:22775410"
/translation="VKNLEQRGNMLHGYFQEAAGEDPQGYENEGDYSESALSN
GANNLYTFLLHHPNLHGGSSILGSLTHLHDLRLA"

ORIGIN

Query Match 46.1%; Score 452.8; DB 8; Length 473;
Best Local Similarity 98.5%; Pred. No. 2.7e-111;
Matches 457; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 459 GGTTAAGAACTTGGAGCAAGAGAGAAACATGCTGATGGCTATTTTGACCAAGAAC 518
DB 1 GGTTAAGAACTTGGAGCAAGAGAGAAACATGCTGATGGCTATTTTGACCAAGAAC 60
QY 519 AGCCGCGAGGATCCACAGTATGTTATGAGGACATGAGGAGACTACGAATCTGCACT 578
DB 61 AGCCGCGAGGATCCACAGTATGTTATGAGGACATGAGGAGACTACGAATCTGCACT 120
QY 579 TGCATTGTCAAAATGGGGCAATAAATCTGTACACTTTCCACCTCCACCCCTTAACCTCA 638
DB 121 TGCATTGTCAAAATGGGGCAATAAATCTGTACACTTTCCACCTCCACCCCTTAACCTCA 180
QY 639 CCACGAGAGAACTCGCTCGGCTCCTCCATCTACTCTGACGATCTCCGCTTGTCTG 698
DB 181 CCACGAGAGAACTCGCTCGGCTCCTCCATCTACTCTGACGATCTCCGCTTGTCTG 240
QY 699 ATCTGATCTGAGATGATTAATCATCACTAAGTTATATATAAGGTCACCTTAACCTG 758
DB 241 ATCTGATCTGAGATGATTAATCATCACTAAGTTATATATAAGGTCACCTTAACCTG 300
QY 759 CTTTGTCTTAAAGTGTGTTGCTTGGTGAATCTCTTTAGGCAAGGATGACCTTGACTA 818
DB 301 CTTTGTCTTAAAGTGTGTTGCTTGGTGAATCTCTTTAGGCAAGGATGACCTTGACTA 360
QY 819 CCTCTGAACACAGATCATATAATATGCTGTGTTTATCAATGATGACACTAAAAA 878

Db 580 AACCTCTATGCATTCCGGCCTGCATCAGGGGCACACCCACC 621

RESULT 7					
GHY9724					
LOCUS	GHY9724	906 bp	mRNA	linear	PLN 02-APR-2003
DEFINITION	Gerbera hybrida cv. 'Terra Regina' mRNA for MADS-box protein, ccd1.				

ACCESSION	GU000724	
VERSION	AJ009724.1	GI:4218168
KEYWORDS	gdef1 gene; MADS-box protein.	
SOURCE	Gerbera hybrid cv. 'Terra Regina'	
ORGANISM	Gerbera hybrid cv. 'Terra Regina'	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Mutisioideae; Mutisieae; Gerbera.	
REFERENCE	1	
AUTHORS	Yu,D., Kotilainen,M., Pollanen,E., Mehto,M., Elomaa,P., Helariutta,Y., Albert,V.A. and Teeri,T.H.	
TITLE	Organ identity genes and modified patterns of flower development in Gerbera hybrida (Asteraceae)	
JOURNAL	Plant J. 17 (1), 51-62 (1999)	
MEDLINE	99168221	
PUBMED	10069067	
REFERENCE	2	(bases 1 to 906)
AUTHORS	Teeri,T.H.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-JUL-1998)	
	University of Helsinki, P.O. Box 56, FIN-00014 Univ. Helsinki, FINLAND	

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FEATURES             source
Location/Qualifiers
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1. .906
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4. .684
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ORIGIN

Query Match	30.3%	Score	297.4	DB	8	Length	906	
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Gaps	2							
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Db	4	ATGGGAGGGGGAAGAT	TAGAT	TAAAGAT	TAGAAAA	CAACAACAGCGCAGGTGACA	63	
QY	61	TACTCAAGAGAGAATAATGGGAT	TCTTCA	GAAGGCTCAG	AGGCTCA	CCGTTCTCTCTGTGAT	120	
Db	64	TACTCAAGAGAGAATAATGGGAT	TATTC	AGAAAGCTCAT	GAACTCA	CTGTTCTTTTGTGAT	123	
QY	121	GCCAAAGGTCCTCCCTCAT	TATGCTCT	CAACACAT	TAAATAAT	GCAACGAGTATATCAGCCCT	180	
Db	124	GCCAAAGTCCTCTCAT	TATGTTCT	CAACACAT	TGGAAAAATTC	CGTGAATATATCAGCCCT	183	
QY	181	ACCCTACGACCAAGAGTAT	TGTANGAT	GACTAT	CAGAAAACTAT	GGGATCGATCTGTGG	240	
Db	184	TCACCTACGACTAAAAAGAT	TGTATGAT	CAGTAC	GACGAGTACT	TAGGGTTTGATCTATGG	243	
QY	241	AGGACACAGGAGGTCGAT	GAAAGACAC	TTGTGGAAGTT	GAAAGAGATCA	CAATTAAG	300	
Db	244	AGTTCTCATATGAGAGGAT	GAAAGGAGACA	ATGAAGAGCT	TAAAGATAC	CCACAATAAA	303	
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Db	304	CTTAGGAGAGAGATCAGG	CAAGAGTTCT	TGTTGAAGATTC	CGATGGTTGGACATGAC	363		
QY	358	GAGCTGGCTTCTTTGAC	ATGATGAGT	CGAGTCTT	CTCTTGGATG	CCCATAGCTCAAGGAAG	417	
Db	364	GATCTCACAGCTCTTGA	ACAACACAT	GCAAGATTC	ACTTTAC	CGTTGTGGGAGAACGAAAG	423	
QY	418	TACCATGTGATCAAAACT	CAGACGGAGAC	CAACAA	GAAAGGTTAAGAACT	TGGAGCAA	477	
Db	424	TACCATGTGATCAAAACT	CAACCCGACA	TTGCAG	AAAAAAGGTTGAGAACT	TTGGAGCAA	483	
QY	478	AGAAGAGGAAAAATGCT	GCATGGCTAT	TTTTTGA	CCAGGAAGC	CGCGGAGGATCCACAG	537	
Db	484	AGAAATGGTAAATCTTC	GCAGTAGACTAT	-----	GAAACAATAC	CAATTTGGATAAAAA	537	
QY	538	TATGGTTATAGGACAAT	CAGGGAGACT	CGAATCT	GCACTTGC	ATTGTCAAATGGGCG	597	
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QY	598	AATAACTTGTAC	CTTTCC	ACTTCC	ACCCTTA	ACCTCCACACGGAG	646	
Db	598	TCAAATCTCTATG	CCCTTTTGTG	ACCCCTTA	CAACATTC	CCCATGGCG	646	

RESULT. T 8

AMDEFI	A.majus deficiens mRNA.	998 bp	mRNA	linear	P.L.N 26-NOV-1992
LOCUS	X52023.1 GI:16019				
DEFINITION	deficiens gene; homeotic flower gene.				
ACCESSION	Antirrhinum majus (snapdragon)				
VERSION	Antirrhinum majus				
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
SOURCE	Magnoliophyta; Eudicotyledons; core eudicots;				
ORGANISM	asterids; Lamiales; Antirrhinaceae; Antirrhineae;				
	Antirrhinum.				
REFERENCE	1 (bases 1 to 998)				
AUTHORS	Sommer,H., Beltran,J.P., Huijser,P., Pape,H., Lonnig,W.E.,				
	Saedler,H. and Schwarz-Sommer,I.				
TITLE	Deficiens, a homeotic gene involved in the control of flower morphogenesis in Antirrhinum majus: the protein shows homology to				


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Qy 652 TCGTCGGCTCCTCCATCTACTCATCT 677
Db 736 TCTGATCTCACCACCTTTTGGCTTGGCT 761

RESULT 9
AF230704 AF230704 994 bp mRNA linear PLN 02-JUN-2000
DEFINITION Petunia x hybrida MADS box transcription factor TM6 mRNA, partial
cds.
ACCESSION AF230704
VERSION AF230704.1 GI:8163949
KEYWORDS
SOURCE
ORGANISM Petunia x hybrida
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.
REFERENCE
1 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Evolution of the petal and stamen developmental programs: Evidence
from comparative studies of the lower eudicots and basal
angiosperms
Int. J. Plant Sci. (2000) In press
2 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Direct Submission
TITLE Submitted (03-FEB-2000) MDSB, Yale University, PO Box 208104, New
Haven, CT 06511-8104, USA
FEATURES
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CDS
ORIGIN
Query Match 28.2%; Score 276.8; DB 8; Length 994;
Best Local Similarity 66.3%; Pred. No. 1.3e-63;
Matches 436; Conservative 0; Mismatches 207; Indels 15; Gaps 2;

Qy 1 ATGGCGCGCGGAAGATTGAATCAAGCTGATCGAAACCAGACCAACAGGCGAGTGAAC 60
Db 1 ATGGGTCTGTGTAATATTGAGATCAAGAAATAGAGAACTCAACAAACAGGCAAGTGA 60

Qy 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCAGCGTTCTCTGTGAT 120
Db 61 TACTCCAAAGAGAAGAAATGGTTATTCAAGAAAGCTAAAGAACTTACTGTCTTCTGTGAT 120

Qy 121 GCCAAGGTCTCCCTCATTATCTCTCCAACTATAATAATGACAGATATATCAGGCCT 180
Db 121 GCTAAGATCTGTCTCATCAUGCTCTCCAGTACTAGGAAATCCATGAGTATACAGTCCC 180

Qy 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAACATATGGGATCGATCTGTGG 240
Db 181 AACACTACGACCAAAAAGATGATTGATTGTACCAAGAGGACACTTGGGGTTGATATTGG 240

Qy 241 AGGCACACAGGAGTCCGATGAAGACACCTTGTGGAGTGTGAAGAGTGAAGAGATCAACAATAG 300
Db 241 AACAGCATTTACGAGAAATCGAGAAACCTTTGACAGATTGAAGAGATATCAATAACAG 300

Qy 301 CTGAGGAGAGAGATCAGGACAGAGTGGGCCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360

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Db 301 CTAAGAAGAGAGATAAGCAAAAGAACAGGGGAGACATGAGCGGCTCAATTTCAGGAA 360
Qy 361 CTGGCTTCTTTGACGATGAGATGCAGTCTTCTTTGGATGCGCATACGTCAAAGGAAGTAC 420
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Qy 481 AGAGGAAACATCTGCATGGCTATTTTGACCAAGGAGAGCGCGGAGGATCCACAGTAT 540
Db 481 CATGGAAGCTCTGTACA-----TGATTTGGAAGCAAAAAGCGAAGATCCAAGTAT 531
Qy 541 GGTATGAGGACAAATGAGGAGACTACGAACTTGCACTTGCATTTCAATGGGCGCAT 600
Db 532 GGTGTAGTGGAAATGAGGAGCAATTTCAACTCTGTATGGCATTTGCCAATGGGTACAC 591
Qy 601 AACTGTGACACTTTCCACCTCCA-----CCACCCTTAACCTCCACACGAGGAGAGCT 652
Db 592 AACCTTTATGCTTTTGGCTACAGAGTGTGACCCCAATCTTCAAAACGAGGAGGAT 649

RESULT 10
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LOCUS
DEFINITION
ACCESSION X60759.1 GI:19385
VERSION MADS box; TDR6 gene.
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 895)
Pnueli, L., Abu-Abeid, M., Zamir, D., Nacken, W., Schwarz-Sommer, Z. and
Lifschitz, E.
The MADS box gene family in tomato: temporal expression during
floral development, conserved secondary structures and homology
with homeotic genes from Antirrhinum and Arabidopsis
Plant J. 1 (2), 255-266 (1991)
93251098
PUBMED 1688249
REFERENCE
2 (bases 1 to 895)
Pnueli, L.
Direct Submission
TITLE Submitted (01-JUL-1991) L. Pnueli, Dept of Biology, Technion-Israel
Inst of Technology, Haifa 32000, ISRAEL
See also X60756-X60760.
LOCATION/Qualifiers
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Matches 418; Conservative 0; Mismatches 204; Indels 9; Gaps 1;

QY 10 GGGAGAGTTGAAATCAAGCTGATCGAAAAACAGACCAACAGGAGGTGACTACTCAAG 69
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DB 62 AGAAGAAACGGTATTTCAAGAAACGTAAGAACTTACTCTTCTGTGACGCTAAGATC 121
QY 130 TCCCTCATTTATGCTCTCAACACCTAATAAATGACGAGTATATCAGCCCTACCACTACG 189
DB 122 TCTCTCATGCTATCAAGCAGGAGTATCATGATGATACAGCCCAACACTACG 181
QY 190 ACCAAGAGTATGATGATGATCACTATCAGAAACCTATGGGATCGATCTGTGGAGGACAC 249
DB 182 ACAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
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DB 482 CTGTGATC-----TTGACTTGGAGAGCAAAATGTGAAGATCCAAAGTATGTTGTG 532
QY 550 GACAATGAGGAGAGACTACGAACTGCACTTGCATTTGCAATGGGCGGAATTAATTTGAT 609
DB 533 GAAATGAGGAGGATTAACCTCTGCTGTGCGCATTTGCGATGAGTACACATCTTTAT 592
QY 610 ACTTTCACCTCCACCACTTACCTCCACC 640
DB 593 GCTTTTCGCTACAACTTGCACCCCAATC 623

RESULT 11

AF230703

LOCUS

DEFINITION

Hydrangea macrophylla MADS box transcription factor TM6 mRNA,

partial cds.

ACCESSION

AF230703

VERSION

AF230703.1

KEYWORDS

GI:8163947

SOURCE

Hydrangea macrophylla

Hydrangea macrophylla

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; Cornales; Hydrangeaceae; Hydrangea.

1 (bases 1 to 939)

REFERENCE

Kramer, E.M. and Irish, V.F.

AU098734

TITLE

Evolution of the petal and stamen developmental programs: Evidence

from comparative studies of the lower eudicots and basal

angiosperms

Int. J. Plant Sci. (2000) In press

REFERENCE

2 (bases 1 to 939)

Kramer, E.M. and Irish, V.F.

AUTHORS

Direct Submission

TITLE

Submitted (03-FEB-2000) MCB, Yale University, PO Box 208104, New

JOURNAL

Haven, CT 06511-8104, USA

FEATURES

Location/Qualifiers

source

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ORIGIN

Query Match 28.0%; Score 275.2; DB 8; Length 939;

Best Local Similarity 70.1%; Pred. No. 3.5e-63;

Matches 405; Conservative 0; Mismatches 158; Indels 15; Gaps 2;

QY 76 AATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGATGCGAGGTCTCCCTC 135

DB 1 AATGGTATAAAGAGAGAGCTCAAGAGCTCACTGTTCTTGTGATGCAAGGTCTCTCTC 60

QY 136 ATTATGCTCTCCACACTAATAAATGACGAGTATATCAGCCCTACCACTACGACCAAG 195

DB 61 ATCATGATCTCCACCACCGCAAGTTCACGAGTACACCACTCCCTCCACCAGCAAA 120

QY 196 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255

DB 121 CAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 256 TCGATGAAGACACCTTGTGAAGTGAAGAGATCAACAATAGCTGAGGAGAGATC 315

DB 181 AGAATGCAAGAACACTTGAAGAGCTGAAGAGGTCAACAACAGCTGAGGAGAGAAATC 240

QY 316 AGGAGAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAGTGGCTTCTCTTTGAC 375

DB 241 AGGAGAGATTTGGGTGAAGATTGAAGCATCTGAACCTTGAATGAACCTGCGTGTATG 300

QY 376 GATGAGATGAGTCTTCTTGGATGCCATCGTCAAGAGAGTACCATGTGATCAAAACT 435

DB 301 CAAAGTCTGCTGCTTCTACTGCTGTCTACCGAAAGAGAGTACCATGTGCTTAAACT 360

QY 436 CAGACGGAGACCAACCAAGAGAGGTTAAGAACTTTGAGCAAAAGAGAGAGAAACATCTG 495

DB 361 CAGACTGAGACTTGCAGGAAGAGTTAGGAACCTTGAAGAGATATGGAATCTTTTC 420

QY 496 CATGCTATTTTTCACGAGGAGACCGCGGAGGATCCACAGTATGTTATGAGGCAAT 555

DB 421 C-----TCGATTTGGAGAGGAAATGTGAAGATCCACAGTACGATTTAGTGGAGAAC 471

QY 556 GAGGAGACTACGAATCTGCATTTGCATTTGCAAAATGGGCGGAATACCTTTGACATTTTC 615

DB 472 GATGAGAGTATGATTTCTGCGTTGCAATTTCCGAATAGGCTCCCGAATTCGTATGCTTTC 531

QY 616 -----CACCTCCACCACTTAACTCCACGAGGAG 647

DB 532 GGGTTGCAACCTACCCACCTTAATCTTTCACCATGGAGG 569

RESULT 12

AY098734

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LOCUS      AY098734      945 bp      mRNA      linear      PLN 17-OCT-2003
DEFINITION Lycopopersicon esculentum TDR6 transcription factor mRNA, partial
cds.
ACCESSION  AY098734
VERSION     AY098734.2  GI:24967131
KEYWORDS
SOURCE      Lycopopersicon esculentum (tomato)
ORGANISM    Lycopopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
            1 (bases 1 to 945)
REFERENCE   Busi,M.V., Bustamante,C., D'Angelo,C., Hidalgo-Cuevas,M.,
            Boggio,S.B., Valle,S.M. and Zabaleta,E.
            MADS-box genes expressed during tomato seed and fruit development
            Plant Mol. Biol. 52 (4), 801-815 (2003)
MEDLINE     22856390
PUBMED      13677468
REFERENCE   2 (bases 1 to 945)
AUTHORS     Busi,M.V., D'Angelo,M.C. and Zabaleta,E.J.
TITLE       Direct Submission
JOURNAL     Submitted (22-APR-2002) Plant Molecular Biology, IIB-INTECH, Camino
            de Circunvalacion de la Laguna Km6, Chascomus, BA 7130, Argentina
3 (bases 1 to 945)
REFERENCE   Busi,M.V., D'Angelo,M.C. and Zabaleta,E.J.
AUTHORS     Direct Submission
JOURNAL     Submitted (14-NOV-2002) Plant Molecular Biology, IIB-INTECH, Camino
            de Circunvalacion de la Laguna Km6, Chascomus, BA 7130, Argentina
REMARK      Sequence update by submitter
COMMENT      On Nov 14, 2002 this sequence version replaced gi:23428889.
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CDS
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            Db      1  GGAATAATTGATCAAGAAGATTGAAACCTTGACAAACCGGCAAGTAATCTTCTCCAAG 60
            Qy      70  AGAAGAAATGGATCTTCAAGAAGGCTCAGAGGTCCCGTCTCTGTGTATGCCAAGTC 129
            Db      61  AGAAGAAACGGTATTTTCAAGAAACGTAAGAACTTACTGTCTTTGTGACGCTAAGATC 120
            Qy      130  TCCCTCATATTGCTCTCCAACTCAATAAAATGACGAGTATATCAAGCCCTACCACTACG 189
            Db      121  TCTCTCATGCTTATCAAGCACCAGGAGTATCATGAGTACACAAGCCCAACACTACG 180
            Qy      190  ACCAAGAGTATGTATGATCATATCAGAAACTATGGGATCGATCTGTGGAGACAC 249
            Db      181  ACAAAGAGATGATTGATCATATCAGATGCACTTGGAGTTCATATCTGGAGCATTCAC 240
            Qy      250  GAGGAGTCGATGAAGACACCTTCTGGAGTTGAAGAGATCAACAATAAGCTGAGAGA 309

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Db      241  TACGAGAAATCAAGAAACTTGAAGAGATTGAAGAGATCAATAACAAGCTAAGAAGA 300
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Db      301  GAGATAAGCCAGAGAACAGGGAAGACATGACGGGACTAAATTTGCAGGAATATGTAC 360
Qy      370  CTTGACGATGAGATGCAAGTCTTCTTGGATGCCATACGTCAAAGGAGTACCATGTGATC 429
Db      361  TTGCAGGAGAACATCACTGAATCTCTGTGAGATTCTGTGACGAAAGTACCACGTGATC 420
Qy      430  AAAAATCGACCGGAGACCAACCAAGAGAGGTTAAGAACTTGGACCAAGAGAGGAAC 489
Db      421  AAGATCAACAGACACCTGCAGAAAGAGCGGAGAACTTAGAAGACAAATGGAAC 480
Qy      490  ATGCTGCATGGCTATTTTGAACAGGAGCAGCGCGGAGGATCCACAGTATGGTTATGAG 549
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Qy      550  GACATGAGGAGACTACGAATCTGCATCTGCAATGTCAATGGGCGGAATACTGTATC 609
Db      532  GAAATGAGGGGCAATTACCACTCTCTGTGGCATTTGGCAATGGAGTACACAATCTTTAT 591
Qy      610  ACTTTCCACCTCCACCAACCCCTAACTCCACC 640
Db      592  GCTTTGGCTACACCATTTGCCACCCCAATC 622

RESULT 13
STPD4
LOCUS     S.tuberosum def4 mRNA for deficiens analogue (clone pd4).
DEFINITION X67508      924 bp      mRNA      linear      PLN 12-JUL-1994
ACCESSION  X67508
VERSION     X67508.1  GI:511064
KEYWORDS    def4 gene; deficiens; MADS-box protein; transcriptional activator.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Solanum.
            1 (bases 1 to 924)
            Garcia-Maroto,F., Salamini,F. and Rohde,W.
            Molecular cloning and expression patterns of three alleles of the
            Deficiens-homologous gene St-deficiens from Solanum tuberosum
            Plant J. 4 (5), 771-780 (1993)
            94100991
            MEDLINE     7903890
            PUBMED
            REFERENCE   2 (bases 1 to 924)
            AUTHORS     Maroto, Salamini and Rohde.
            JOURNAL     Unpublished
            REFERENCE   3 (bases 1 to 924)
            AUTHORS     Garcia-Maroto,F.
            TITLE       Direct Submission
            JOURNAL     Submitted (24-AUG-1992) F. Garcia-Maroto, MPI f
            Zuechtungsforshung, Carl-von-Linne-Weg 10, 5000 koeln 30, FRG
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Best Local Similarity 63.7%; Pred. No. 1.3e-57;
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ACCESSION AB071378
VERSION AB071378.1
KEYWORDS GI:20513259
SOURCE Liliun regale
ORGANISM Liliun regale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Lilium.
REFERENCE
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AUTHORS Winter,K.U., Weiser,C., Kaufmann,K., Bohne,A., Kirchner,C.,
Kanno,A., Saedler,H. and Theissen,G.
TITLE Evolution of class B floral homeotic proteins: obligate
heterodimerization originated from homodimerization
JOURNAL Mol. Biol. Evol. 19 (5), 587-596 (2002)
MEDLINE 21959322
PubMed 11961093
REFERENCE
2 (bases 1 to 1005)
AUTHORS Kanno,A., Bohne,A., Saedler,H. and Theissen,G.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail:kanno@ige.tohoku.ac.jp,
Tel:81-22-217-5725(ex.5725), Fax:81-22-217-5725)
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Best Local Similarity 58.2%; Pred. No. 5.6e-56;
Matches 456; Conservative 0; Mismatches 324; Indels 3; Gaps 1;

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 ACCESSION AF503913.1 GI:20531752
 VERSION AF503913.1
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 Lilium.
 1 (bases 1 to 1039)
 Tzeng,T.Y. and Yang,C.H.
 A MADS box gene from lily (Lilium longiflorum) is sufficient to
 generate dominant negative mutation by interacting with PISTILLATA
 (PT) in Arabidopsis thaliana
 (PT) in Arabidopsis thaliana
 Plant Cell Physiol. 42 (10), 1156-1168 (2001)
 JOURNAL MEDLINE 21530302
 PUBMED 11673632
 REFERENCE 2 (bases 1 to 1039)
 Tzeng,T.-Y. and Yang,C.-H.
 Direct Submission
 TITLE Submitted (18-APR-2002) Institute of Biotechnology, National Chung
 Hsing University, 250 Kao-Kung Rd., Taichung, Taiwan 40227, ROC
 JOURNAL Location/Qualifiers
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Query Match

24.8%; Score 244; DB 8; Length 1039;

Best Local Similarity 62.9%; Pred. No. 9.9e-55;
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GenCore version 5.1.6
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Run on: September 26, 2004, 05:39:13 ; Search time 66.8568 Seconds
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Title: US-10-069-527-2

Perfect score: 1103

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	346	31.4	1345	3	US-09-149-976-7
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ALIGNMENTS

RESULT 1

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; Sequence 3, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-09-410-464-3

Alignment Scores:
Pred. No.: 1.32e-33
Score: 358.00
Percent Similarity: 57.94%
Best Local Similarity: 38.79%
Query Match: 32.46%
DB: 4
Length: 681
Matches: 83
Conservative: 41
Mismatches: 82
Indels: 9
Gaps: 2

US-10-069-527-2 (1-215) x US-09-410-464-3 (1-681)

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RESULT 2

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 ; Patent No. 6395892
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; FILE REFERENCE: 53375
 ; CURRENT APPLICATION NUMBER: US/09/410,464
 ; CURRENT FILING DATE: 1999-10-01
 ; EARLIER APPLICATION NUMBER: 09/287,700
 ; EARLIER FILING DATE: 1999-04-06
 ; EARLIER APPLICATION NUMBER: 60/080,851
 ; EARLIER FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
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 ; SEQ ID NO 2
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 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(684)
 ; US-09-410-464-2

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 Score:

Percent Similarity: 57.94% Conservative: 41
 Best Local Similarity: 38.79% Mismatches: 82
 Query Match: 32.46% Indels: 9
 DB: Gaps: 2

US-10-069-527-2 (1-215) x US-09-410-464-2 (1-946)

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 QY 61 SerThrThrLeuThrGluLeuLeuAspLysTyrHisGlyGlnSerGlyLysLeuTrp 80
 Db 181 TCCACATCGAAGAGAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240
 QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAsnAspSer 100
 Db 241 GGCACTCAATACAGAAATGCAAGAGCACTTGAGGAAGCTGAATGATATCAATCAATAG 300
 QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 Db 301 CTGAGCAAGAAATCAGGAGAGGAGAGAGGCGCTGAATGATCTGAGCATTCATCAT 360
 QY 121 LeuMetAlaLeuGluLalaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
 Db 361 CTGCGCGGTCTTGAGCAACATATGATGAAAGCTTGAATGGTGGCGGAGGAAGTAC 420
 QY 141 LysPheVal-----AspMetMetArgAspAsnGlyLysAlaLeuGluAspGlu 156
 Db 421 CATGTGATCAAAACACAAACGAACTACAGGAAGAGTGAAGAAATTTAGAGGAGAGA 480
 QY 157 AsnLysArgLeuThrTyrGluLeuGlnLysGlnGluMetLysIleLeuLysGluAsnVal 176
 Db 481 CATGAAACCTCTTGATGGAA-----TATGAAGCAAACTAGAGGATCGACAG 528
 QY 177 ArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGln 196
 Db 529 TATGGTTTATGGCAATGAAGCTGCTGTTCACCTTGCAATGGGCTTCCACCTCTAT 588
 QY 197 GlnIleProPheAlaPheArgValGlnProAsn 210
 Db 589 GC-ATTCGCGCTGCATCAGCGGCAACACCAACCACTCT 629

RESULT 3

US-08-592-214A-7
 ; Sequence 7, Application US/08592214A
 ; Patent No. 5815336
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
 ; TITLE OF INVENTION: Genes and Methods of Using Same
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

D_b 149 ATGGGGCGGGCAAGGTACAGCTGAAGCGGATAGAGAAACAAGATAAACCGGCAGGTGACC 208

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QY 21 TyrSerLysArgAsnGlyLeuLeuLysAlaLysGluLeuThrValLeuCysAsp 40
Db 209 TTCTCCAAAGCGCGAAGCGCTGCTCAAGAAGGCGCAGAGATCTCGGTCTCTGCGAT 268
QY 41 AlaLysValSerLeuLeuLeuLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 269 GCGAGGTGCGGTCTGCTCTCTCCCAAGGCGAGCTCTACAGTACGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78
Db 329 TCC---CGCATGACAAATTTCTTGAACGCTATGACGATATTCCTATGCTGAAAGGCT 385
QY 79 LeuTrpAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
Db 386 CTATTATTCAGCTGAATCTGAAAGTGAGGGAATTTGTCACCAATACAGAACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspLeuThrSer 115
Db 446 GCCAAAATTGAGACCATACAAAATGCCACCAACCTGATGGAGAGGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135
Db 506 TTGAATCCCAAGAGCTCCAGCAACTAGACGAGCTGGATAGCTCACTGAAGCACATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
Db 566 AGATCAAGGAGAGCCACCTTATGGCCGAGTCTATTCTGAGCTACAGAGAGGAGG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 173
Db 626 TCACTGAGGAGAGACAGAGGCTCTGCAGAAAGAACTTGGGAGGAGGAGGCGGCTC 685
QY 165 -----GlnLysGlnGlnMetLysIle-----Lys 173
Db 686 GCGAGCGGCGAGCAGCAACAGCAGCAGCTGAGTGGGAGGAGGAGGAGGAGGAGG 745
QY 174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsn 193
Db 746 GCCCAGACAGCTCATCTGCTCTCTCTCATGATGAGGAGG-----787

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RESULT 5

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US-08-655-227-7
Sequence 7, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin P.
TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays API."
US-08-655-227-7
Alignment Scores:
Pred. No.: 8,21e-32 Length: 1345
Score: 346.00 Matches: 83
Percent Similarity: 59.29% Conservative: 51
Best Local Similarity: 36.73% Mismatches: 58
Query Match: 31.37% Indels: 34
DB: 3 Gaps: 7
US-10-069-527-2 (1-215) x US-08-655-227-7 (1-1345)
QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 149 ATGGGGCGCGCAAGGTACAGCTGAAGCGGATAGAGAACAAGATAACCGCGAGGTGACC 208
QY 21 TyrSerLysArgAsnGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 40
Db 209 TTCTCCAAAGCGCGAAGCGCTGCTCAAGAAGGCGCAGAGATCTCGGTCTCTGCGAT 268
QY 41 AlaLysValSerLeuLeuLeuLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 269 GCGAGGTGCGGTCTGCTCTCTCCCAAGGCGAGCTCTACAGTACGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78
Db 329 TCC---CGCATGACAAATTTCTTGAACGCTATGACGATATTCCTATGCTGAAAGGCT 385
QY 79 LeuTrpAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
Db 386 CTATTATTCAGCTGAATCTGAAAGTGAGGGAATTTGTCACCAATACAGAACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspLeuThrSer 115
Db 446 GCCAAAATTGAGACCATACAAAATGCCACCAACCTGATGGAGAGGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135
Db 506 TTGAATCCCAAGAGCTCCAGCAACTAGACGAGCTGGATAGCTCACTGAAGCACATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
Db 566 AGATCAAGGAGAGCCACCTTATGGCCGAGTCTATTCTGAGCTACAGAGAGGAGG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 164
Db 626 TCACTGAGGAGAGACAGAGGCTCTGCAGAAAGAACTTGGGAGGAGGAGGCGGCTC 685
QY 165 -----GlnLysGlnGlnMetLysIle-----Lys 173
Db 686 GCGAGCGGCGAGCAGCAACAGCAGCAGCTGAGTGGGAGGAGGAGGAGGAGGAGG 745
QY 174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsn 193
Db 746 GCCCAGACAGCTCATCTGCTCTCTCTCATGATGAGGAGG-----787

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QY 194 AsnGlnGlnGlnPro 199
Db 788 GATCAGCAGGACTGCGG 805

RESULT 6
US-08-655-241-7
; Sequence 7, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1345
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays APL."
US-08-655-241-7

Alignment Scores:
Pred. No.: 8,21e-32 Length: 1345
Score: 346.00 Matches: 83
Percent Similarity: 59.29% Conservative: 51
Best Local Similarity: 36.73% Mismatches: 58
Query Match: 31.37% Indels: 34
DB: Gaps: 7

US-10-069-527-2 (1-215) x US-08-655-241-7 (1-1345)
QY 1 MetGlyArgGlyValGluLeuLysArgGluAsnSerSerAsnArgGlnValThr 20
Db 149 ATGGGGCGCGCAAGTACGTGTAAGCGGATAGAACAAAGTAAACCGCGAGTGACC 208
QY 21 TyrSerLysArgAsnGlyLleLysLysAlaLysGluLeuThrValLeuCysAsp 40
Db 209 TTCTCCAAAGCGCGCAAGCGCTGCTCAAGAGGCGCAGAGATCTCCGCTCTCGCAT 268
QY 41 AlaLysValSerLeuLleLysTyrSerSerGlyLysMetValGluLysTyrCysSerPro 60
Db 41 AlaLysValSerLeuLleLysTyrSerSerGlyLysMetValGluLysTyrCysSerPro 60

269 GCCAGGTGCGCGTATCGTCTTCTCCCAAGGCAAGCTTACGAGTAGCCACCGAC 328
61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLys 78
329 TCC---CGCATGGACAAAATCTTGAACGCTATGAGCGATATCTCTATGCTGAAAAGGCT 365
79 LeuTrpAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
386 CTATTTCAGCTGAATCTGAAAGTGAGGAAATTTGGTCCACGAATACAGGAAACTGAAG 445
96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspLleThrSer 115
446 CCAAAAATTGAGACCATACAAAAATGCCAAGACACCTGATGGGAGAGGATCTAGAGTCT 505
116 LeuAsnHisValGluLeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIle 135
506 TTGAATCCCAAGAGCTCCAGCAACTAGACGACGAGCTGGATAGCTCACTGAACACATC 565
136 ArgAspLysGlnSer-----LysPheValAspMetMetMetArgAspAsnGlyLys 151
566 AGATCAAGAGAGAGCCACCTTATGGCGAGTCTATTTCTGAGCTACAGAAGAGGAGG 625
152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 164
626 TCACTGACGAGGAGAACAGGCTCTGCAGAGGAATTTGGGAGAGCGAGAGCGCGTC 685
165 -----GlnLysGlnGlnMetLysIle-----Lys 173
686 GCGAGCGCGCAGCAGCAGCAACAGCAGCGTGCAGTGGGACCAAGACACATGCCCCAG 745
174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsn 193
746 GCCAGACAAGCTCATCGTCTCTCTTCATGATGAGCGAG-----Lys 787
194 AsnGlnGlnGlnIlePro 199
788 GATCAGCAGGACTGCGG 805

RESULT 7
US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
```

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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1345
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays APl."
; US-09-149-976-7

Alignment Scores:
Pred. No.:      8 21e-32      Length:      1345
Score:          345.00      Matches:      83
Percent Similarity: 59.29%      Conservative: 51
Best Local Similarity: 36.73%      Mismatches: 58
Query Match:      31.37%      Indels:      34
DB:              7          Gaps:          7

US-10-069-527-2 (1-215) x US-09-149-976-7 (1-1345)

QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
DB 149 ATGGGGCGCGCGAGGTACAGCTGAAGCGGAGTAGAGAACAGATAACCGCGAGGTGACC 208
QY 21 TyrSerLysArgArgAsnGlyIleLysLysAlaLysGluLeuThrValLeuCysAsp 40
DB 209 TTCTCCAGCGCGGACCGCTGCTCAGAGGCGCAGAGATCTCGTCTCTCGCAT 268
QY 41 AlaLysValSerLeuLeuLysTyrSerSerGlyLysMetValGluTyrCysSerPro 60
DB 269 GCCGAGTGGCGCTCATCGTCTCTCCCGAGGCGAGCTACGAGTACGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78
DB 329 TCC---CGATGGACAAATCTTGACCGCTATGACCGATATCTCTATGCTGAAAGGCT 385
QY 79 LeuTrpAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
DB 386 CTATTTCAGCTGAATCTGAAAGTGAGGGAATTTGTGCCAGCATACAGGAAGACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSer 115
DB 446 GCCAAATTTGAGACCATACAAAATGCCCAAGCACCTGATGGGAGAGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135
DB 506 TTGAATCCCAAGAGCTCCAGCAACTAGAGCAGCTGGATAGCTCACTGAAGCACATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
DB 566 AGATCAAGGAAGAGCACCTTATGGCCGAGTCTATTCTGAGCTACAGAGAAGGAGGAG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu----- 164
DB 626 TCACTCGAGGAGAGAACAGGCTCTGCAGAGGAACTTCGGGAGGAGCAGAGCCGCTC 685
QY 165 -----GlnLysGlnGlnGluMetLysIle-----Lys 173
DB 686 GCGAGCGCGGAGCAGCAGCAACAGCAGCAGGCTGAGTGGGACAGCAGACATGCCCGAC 745
QY 174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAen 193
DB 746 GCCACAGACAGCTCATCATGCTCTCTCTCATGATGAGGACAG----- 787
QY 194 AsnGlnGlnGlnIlePro 199
DB 788 GATCAGCAGGAGTGGCG 805

RESULT 8
US-09-398-326-7
; Sequence 7, Application US/09398326
; Patent No. 635863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/659,188
; APPLICATION NUMBER:
; FILING DATE: 05-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 149..968
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays APl."
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QY	205	GlnProIleGlnProAsnLeuGlnGluArgTle 215	1062
Db	707	ACCTCTCCAGAGATGGCTTTTGTGGAGAGAGTT 739	
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US-09-105-652-1	US-09-105-652-1		
Sequence 1, Application US/09105652	Sequence 1, Application US/09105652		
Patent No. 6229088	Patent No. 6229088		
GENERAL INFORMATION:	GENERAL INFORMATION:		
APPLICANT: Yanofsky, Martin F.	APPLICANT: Yanofsky, Martin F.		
APPLICANT: Martienssen, Robert	APPLICANT: Martienssen, Robert		
APPLICANT: Ferrandiz, Cristina	APPLICANT: Ferrandiz, Cristina		
APPLICANT: Gu, Qing	APPLICANT: Gu, Qing		
TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant	TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant		
FILE REFERENCE: P-UD 3040	FILE REFERENCE: P-UD 3040		
CURRENT APPLICATION NUMBER: US/09/105,652	CURRENT APPLICATION NUMBER: US/09/105,652		
CURRENT FILING DATE: 1998-06-26	CURRENT FILING DATE: 1998-06-26		
EARLIER APPLICATION NUMBER: 60/051,030	EARLIER APPLICATION NUMBER: 60/051,030		
EARLIER FILING DATE: 1997-06-27	EARLIER FILING DATE: 1997-06-27		
NUMBER OF SEQ ID NOS: 4	NUMBER OF SEQ ID NOS: 4		
SOFTWARE: Patentin Ver. 2.0	SOFTWARE: Patentin Ver. 2.0		
SEQ ID NO 1	SEQ ID NO 1		
LENGTH: 1062	LENGTH: 1062		
TYPE: DNA	TYPE: DNA		
ORGANISM: Arabidopsis sp.	ORGANISM: Arabidopsis sp.		
FEATURE:	FEATURE:		
NAME/KEY: CDS	NAME/KEY: CDS		
LOCATION: (101)..(826)	LOCATION: (101)..(826)		
FEATURE:	FEATURE:		
NAME/KEY: polyA signal	NAME/KEY: polyA signal		
LOCATION: (1061)	LOCATION: (1061)		
US-09-105-652-1	US-09-105-652-1		
Alignment Scores:	Alignment Scores:		
Pred. No.:	4,748-30	Length:	1062
Score:	330.00	Matches:	83
Percent Similarity:	55.84%	Conservative:	46
Best Local Similarity:	35.93%	Mismatches:	68
Query Match:	29.92%	Indels:	34
DB:	3	Gaps:	7
US-10-069-527-2 (1-215) x US-09-105-652-1 (1-1062)	US-10-069-527-2 (1-215) x US-09-105-652-1 (1-1062)		
QY	1	MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20	
Db	101	ATGGGAAGAGGTAGGTTTCAGCTGAAGAGATAGAGAACAGATCAATAGGCAAGTTACT 160	
QY	21	TyrSerLysArgAsnGlyLleLysLysAlaLysGluIleThrValLeuCysAsp 40	
Db	161	TTCTCAAGAGAAGGTCTGGTTGTCTCAGAAAGCTCATGAGATCTCTGTTCTGGCAT 220	
QY	41	AlaLysValSerLeuIleLysSerSerGlyLysMetValGluLysCysSerPro 60	
Db	221	GCTGAGTTGCTCTCATCT 277	
QY	61	SerThrThrLeuThrGluLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78	
Db	278	GACTCTTGATGGAGAGATCTTGAACGCTATGCTGCTATTTATATTATTCAGACAA 337	
QY	79	Leu-----TyrAspAlaLysHisGluAsnLeuSer 88	
Db	338	CTTGTGGCGGACGCTTTCACAAAGTGAATAATGGTCTTGAACATGCTAAGCTCAAG 397	
QY	89	AsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeu 108	
Db	398	GCAAGAGTTGAGTACTTTCAGAGAACAAA-----AGGAATTTT 436	
QY	109	LysGlyGluAspLleThrSerLeuAsnHisValGluLeuMetAlaLeuGluAlaLeu 128	
Db	437	ATGGGGGAAGATCTTCAATCGTTGAGCTTGAAGGAGCTTCAAGAGCTTGAGCATCAGCTC 496	
QY	129	GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValAsp 144	

OTHER INFORMATION: Amino Acid Sequences of the AGL8 cDNA clone."
US-09-349-677-1

Alignment Scores: 4.74e-30 Length: 1062
Pred. No.: 330.00 Matches: 83
Percent Similarity: 55.84% Conservative: 46
Best Local Similarity: 35.93% Mismatches: 68
Query Match: 29.92% Indels: 34
DB: Gaps: 7

US-10-069-527-2 (1-215) x US-09-349-677-1 (1-1062)

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QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
DB 101 ATGGGAAGAGGTAGGTTGCTGCTGAGGATGAGAGACAGATCAATAGGCAAGTTACT 160
QY 21 TyrSerLysArgAsnGlyLeuLysLysLysLysLysLysLysLysLysLysLysLys 40
DB 161 TTCTCAAGAGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220
QY 41 AlaLysValSerLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 60
DB 221 GCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
QY 61 SerThrThrLeuThrGluLeuLysLysLysLysLysLysLysLysLysLysLysLys 78
DB 278 GACTCTTGATGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337
QY 79 Leu-----TTPAspAlaLysHisGluAsnLeuSer 88
DB 338 CTGTTGGCGGACGCTTTCACAAAGTGAAATGGTCTTAGAACATGCTAAGCTCAAG 397
QY 89 AsnGluValAspArgValLysLysLysLysLysLysLysLysLysLysLysLysLys 108
DB 398 GCAAGAGTTGAGGTACTTGAGAGAACAAA-----AGGAATTTT 436
QY 109 LysGlyGlnGluMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 128
DB 437 ATGGGGAGAGTCTGATTCGTTGAGCTTGAAGAGCTCCAAAGCTTGAGCATCAGCTC 496
QY 129 GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValAsp 144
DB 497 GATGCAGCTATCAAGAGCATTAGTGTCAAGAAAGAACCAAGCTATGTTGCAATCATCT 556
QY 145 MetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrThrGluLeu 164
DB 557 GCGCTCCAGAGAGGATTAAGCTTTCAGAGCTTCAAGAGCTCCAAAGCTTGAGCATCAGCTC 607
QY 165 GlnLysGlnGlnMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 184
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DB 647 GAAGGACAATTAGTCCAAATGCTCCAACTCTTTCAGTTCTTCTGCTCCAACTACTGCGTA 706
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RESULT 14

US-09-708-584-1
; Sequence 1, Application US/09708584
; Patent No. 6541683
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Martensen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/708,584

; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/105,652
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/051,030
; PRIOR FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(826)
; NAME/KEY: polyA signal
; LOCATION: (1061)
US-09-708-584-1
Alignment Scores: 4.74e-30 Length: 1062
Pred. No.: 330.00 Matches: 83
Percent Similarity: 55.84% Conservative: 46
Best Local Similarity: 35.93% Mismatches: 68
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US-10-069-527-2 (1-215) x US-09-708-584-1 (1-1062)

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DB 221 GCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
QY 61 SerThrThrLeuThrGluLeuLysLysLysLysLysLysLysLysLysLysLysLys 78
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QY 79 Leu-----TTPAspAlaLysHisGluAsnLeuSer 88
DB 338 CTGTTGGCGGACGCTTTCACAAAGTGAAATGGTCTTAGAACATGCTAAGCTCAAG 397
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QY 129 GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValAsp 144
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Db 707 ACCTCTCAGAGATGGCTTTGGAGAGATT 739
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US-08-485-981-9
; Sequence 9, Application US/08485981
; Patent No. 5861542
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND
; TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,981
; FILING DATE: June 7, 1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-42933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-485-981-9

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Query Match: 29.15% Indels: 25
DB: 2 Gaps: 6

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Db 193 AGCTTAGCATGCTCAAGACATTAGAGAGGTACCAG-----AAGTGCACACTAC 240
Qy 81 AspalalysHisGluAsnLeuSer-----AsnGlu 90
Db 241 GGAGCACACAGAGACCAATATATCCACACGAGAACACTGGAAATAAGTAGCAACACAGAA 300
Qy 91 ValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGly 110
Db 301 TACTTGAAGCTTAAGACAGCTTACGAGCATTCAGCGCATCACAGAGAAATCTTCTTGGT 360
Qy 111 GluAspIleThrSerLeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsn 130
Db 361 GAAGATCTTGGCCCTTTGATAGCAAGAACTTGAATCATTGAGAGCGACCTTGATGATG 420
Qy 131 GlyLeuThrSerIleArgAspLysGlnSerLys---PheValAspMetMetArgAsp--- 148
Db 421 TCACGTGAACACAGATTCGATCACTCGGACTCAGTTAATGTTGGATCAACTTACAGATCTT 480
Qy 149 -----AsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeuGlnLys 166
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Qy 167 GlnGlnGluMetLysIleLysGluAsnValArgAsnMetGluAsnGlyTyrHisGlnArg 186
Db 541 GGAAGCCCAACTAAATCTCGAGTGGCAACAAATGCACAGATATGGCTACGGCGGCA 600
Qy 187 GlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPheAlaPheArgValGlnPro 206
Db 601 -----ACAACTCAAACTCAGGGCGATGGCTTTTTCATCCTTTGGAA 642
Qy 207 IleGlnProAsnLeuGln 212
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Job time : 69.8568 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 04:52:23 ; Search time 3674.24 Seconds
(without alignments)
2536.240 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	975	88.4	890	8	AB081092	AB081092 Malus x d
3	824	74.7	845	8	AF043255	AF043255 Cucumis s
4	811	73.5	967	8	AB038462	AB038462 Rosa rugo
5	740.5	67.1	971	8	PHFMADS2	X69947 P.hybrida m
6	739.5	67.0	904	8	PHFBP3	X71417 P.hybrida f
7	720	65.3	875	8	AF488589	AJ488589 Betula p
8	707	64.1	768	8	NTGLOBOSA	B67959 N.tabacum G
9	701.5	63.6	822	8	AB071379	AB071379 Lilium re
10	698.5	63.3	761	8	AF230711	AF230711 Hydrangea
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12	696	63.1	876	8	AB094967	AB094967 Tulipa ge
13	691	62.6	810	8	GHY9726	AJ009726 Gerbera h
14	685.5	62.1	814	8	AY173061	AY173061 Chrysanth
15	684.5	62.1	780	6	A36587	A36587 Sequence 1
16	684.5	62.1	780	8	PRTTNSPA	M91190 Petunia tra
17	684	62.0	896	8	SLSLM2	X80489 S.latifolia
18	669.5	60.7	920	8	AF029976	AF029976 Eucalyptu
19	666	60.4	888	8	AF134114	AF134114 Hyacinthu
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22	663.5	60.2	959	8	AF230710	AF230710 Chloranth
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24	660.5	59.9	896	8	ATHMADSBOX	D30807 Arabidopsis
25	647	58.7	802	8	AF052862	AF052862 Delphinu
26	643	58.3	801	8	AB071380	AB071380 Lilium re
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ALIGNMENTS

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 DEFINITION Malus domestica mRNA for Pistillata MADS-box protein (pi gene).
 ACCESSION AJ291490
 VERSION AJ291490.1 GI:12666532
 KEYWORDS PI gene; Pistillata MADS-box protein.
 SOURCE Malus x domestica (apple tree)
 ORGANISM Malus x domestica
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 AUTHORS Yao, J., Dong, Y. and Morris, B.A.
 TITLE Parthenocarpic apple fruit production conferred by transposon
 insertion mutations in a MADS-box transcription factor
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)
 MEDLINE 21107711
 PUBMED 11158635
 REFERENCE 2 (bases 1 to 868)
 AUTHORS Yao, J.L.
 TITLE Direct Submission
 JOURNAL Submitted (16-OCT-2000) Yao J.L., Plant Health and Development
 Group, Horticulture and Food Research Institute of New Zealand, 120
 Mc Albert Road, Auckland, Private Bag 92169, NEW ZEALAND
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 Qy 41 AlaLysValSerLeuIleLysTyrSerSerSerGlyLysMetValGluTyrCysSerPro 60
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 Qy 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle 215
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 RESULT 2
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 DEFINITION Malus x domestica MdPI mRNA for MADS-box protein, partial cds.
 ACCESSION AB081092
 VERSION AB081092.1 GI:22775405
 KEYWORDS Malus x domestica (apple tree)
 SOURCE Malus x domestica
 ORGANISM Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 AUTHORS Matsumoto, S., Ohtsubo, T. and Soejima, J.
 TITLE Cloning and sequencing of apple MADS-box genes 'MdPI', 'MDTM6', and
 'MdIMADS13'
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 890)
 AUTHORS Ohtsubo, T. and Matsumoto, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
 Department of Biology, Faculty of Education, 1-1, Yanagido, Gifu,
 Gifu 501-1193, Japan (E-mail:shmatsumo@gifu-u.ac.jp,
 Tel:81-58-293-2257, Fax:81-58-293-2207)
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ORIGIN

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 Best Local Similarity: 99.47% Mismatches: 0
 Query Match: 88.40% Indels: 0
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US-10-069-527-2 (1-215) x AB081092 (1-890)

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 Db 542 CCTATTTCAGCAAAATCTCCAGGAGAAATC 571

RESULT 3

AF043255
 LOCUS 845 bp mRNA linear PLN 05-JAN-1999
 DEFINITION Cucumis sativus MADS box protein 26 (CUM26) mRNA, complete cds.
 ACCESSION AF043255
 VERSION AF043255.1 GI:4105096

KEYWORDS

Cucumis sativus (cucumber)

Cucumis sativus

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

1 (bases 1 to 845)

Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and Angenent,G.C.

Class C homeotic genes are required for whorl specific sex

determination in unisexual flowers

REFERENCE

2 (bases 1 to 845)

Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and Angenent,G.C.

TITLE

JOURNAL

Submitted (15-JAN-1998) Developm. Biology, CPRO-DLO,
 Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands

FEATURES

Source

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CDS

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ORIGIN

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 Best Local Similarity: 73.83% Mismatches: 18
 Query Match: 74.71% Indels: 4
 DB: 8 Gaps: 2

US-10-069-527-2 (1-215) x AF043255 (1-845)

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 QY 21 TyrSerLysArgAsnGlyLysIleLysLysLysLysLysLysLysLysLysLysLysLys 40
 Db 66 TATTCAAAGAGAGAAATGGTATCATCAAAAGAACCAAGAAATATCTGTTCTTTGGCAT 125
 QY 41 AlaLysValSerLeuIleLysTyrSerSerSerGlyLysMetValGluTyrCysSerPro 60
 Db 126 GCTCAAGTTCTTGTGTCATTTTGTAGCTCTGGAATAATGCATGAATATTGACGCCCT 185
 QY 61 SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80
 Db 186 TCTACACCTTTGGTTGATATCTTGGATAAGTATCACAAGCAATCTGGGAAGAGGCTGTG 245
 QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
 Db 246 GATGCTAAGCATGAGATCTGAGCAATGAAATGATAGAGTTAAGAAAGAGATGACAAC 305
 QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 Db 306 ATGCAGATTGAGCTAAGGCATTTGAGAGAGAGATATAACGCTCTTTGAACATACAAGGAG 365
 QY 121 LeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
 Db 366 TTAATGAGCTCTGAGAGAGAGCTCTTGAATAATGGCCTCACCGGTGTTCGTGAGAGACATCG 425
 QY 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
 Db 426 GAATTCATGAAATGATGAGACAAATGAAAGAAATGATGGAAGAGAGAGAAACAAGCGCCTT 485
 QY 161 ThrThrGluLeuGlnLysGlnGlnMetLysIleLysGluAsnValArgAsnMetGlu 180
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ORIGIN
Alignment Scores:
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Score: 740.50 Matches: 145
Percent Similarity: 81.86% Conservative: 31
Best Local Similarity: 67.44% Mismatches: 36
Query Match: 67.14% Indels: 3
DB: 8 Gaps: 1

US-10-069-527-2 (1-215) x PHPMADS2 (1-971)

Qy 1 MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 45 ATGGGAGAGAGAAAGATAGAGATAAAGAGAAATAGAGAACTCTAGCAACAGCAAGTTACT 104
Qy 21 TyrSerLysArgArgAsnGlyIleLysLysAlaLysGluIleThrValLeuCysAsp 40
Db 105 TACTCCAGAGAGAAATGGGATATCAAGAAAGCTAAGAAATCACTGTTCTTTGTGAT 164
Qy 41 AlaLysValSerLeuIleLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 165 GCTAAGGTTTCCCTTATCATCTTTGTTGTAATCTCGCAAGATGATCAATATTGTAGCCCT 224
Qy 61 SerThrThrLeuThrGluIleLysLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80
Db 225 TCTACTACGTTACTGATGCTGATGCTGATGCTTCAAAAACCTTCTGGAGGAGGCTATGG 284
Qy 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
Db 285 GATGCTAAGCATGAGAACTTGAGCAATGAAATCGATAGATCAAGAAAGAGAACGACAT 344
Qy 101 MetGlnValGluLeuArgHisLeuLysGlyLysIleThrSerLeuAsnHisValGlu 120
Db 345 ATGCAAGTTAAGCTCAGGCACCTCAAGAGGAGAGATATCAATCTTTGAACACCAAGAG 404
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Qy 161 ThrTyrGluLeuGlnLysGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
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Qy 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnIleProPhe 200
Db 585 GAAGTGATCATCAAAAGAGGATGGGAGGATGATGATGATGATGATGATGATGATGATGAT 635
Qy 201 AlaPheArgValGlnProLysGlnProAsnLeuGlnGluArgIle 215
Db 636 GCCCTTCGAGTTTCAGCAATGAGCCAAATCTACATGAAAGAGATG 680

RESULT 6
PHEBP3 904 bp mRNA linear PLN 10-FEB-1994
LOCUS

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DEFINITION P.hybrida fbp3 mRNA.
ACCESSION X71417
VERSION X71417.1 GI:454264
KEYWORDS fbp3 gene; MADS-box protein.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Petunia.

REFERENCE
AUTHORS Angenent,G.C., Franken,J., Busscher,M., Weiss,D. and van Tunen,A.J.
TITLE Co-suppression of the petunia homeotic gene fbp2 affects the
 identity of the generative meristem
JOURNAL Plant J. 5 (1), 33-44 (1994)
MEDLINE 94177174
PUBMED 7907515

REFERENCE 2 (bases 1 to 904)
AUTHORS Angenent,G.C.
TITLE Direct Submision
JOURNAL Submitted (30-MAR-1993) G.C. Angenent, CPRO-DLO, Droevendaalsesteeg
 1, Wageningen, THE NETHERLANDS
FEATURES Location/Qualifiers
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 strain="R27"
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ORIGIN
 Alignment Scores:
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 Score: 739.50 Matches: 145
 Percent Similarity: 81.86% Conservative: 31
 Best Local Similarity: 67.44% Mismatches: 36
 Query Match: 67.04% Indels: 3
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 US-10-069-527-2 (1-215) x PHEBP3 (1-904)

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 Qy 21 TyrSerLysArgArgAsnGlyIleLysLysAlaLysGluIleThrValLeuCysAsp 40
 Db 106 TACTCCAGAGAGAAATGGGATATCAAGAAAGCTAAGAAATCACTGTTCTTTGTGAT 165
 Qy 41 AlaLysValSerLeuIleLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
 Db 166 GCTAAGGTTTCCCTTATCATCTTTGTTGTAATCTCGCAAGATGATCAATATTGTAGCCCT 225
 Qy 61 SerThrThrLeuThrGluIleLysAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80
 Db 226 TCTACTACGTTACTGATGCTGATGCTGATGCTTCAAAAACCTTCTGGAGGAGGCTATGG 285
 Qy 81 AspAlaLysHisGluAsnLeuSerAsnGluValArgValLysLysAspAsnAspSer 100
 Db 286 GATGCTAAGCATGAGAACTTGAGCAATGAAATCGATAGATCAAGAAAGAGAACGACAT 345

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QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
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QY 121 LeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
Db 406 CTTATGTTTGGAGAAGCTTAACAAATGACATTTCTAGTATCAGTGCCAGCAGTCG 465
QY 141 LysPheValAspMetMetArgAspLysGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
Db 466 GAGATCTTGGATATGATCAGGAAATATGATCAATTTCTGGAGGAGGACACAACTT 525
QY 161 ThrTyrGluLeuGlnLysGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
Db 526 CATATGCTTTGCACCAAGAGGATGGCAGCATGGGTGGAATATGAGATGATGAA 585
QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPhe 200
Db 586 GAAGTGTACCATCAAGA-----GACAGGATAGCAATACACAGCAGATGCCATT 636
QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle 215
Db 637 GCCCTTCGAGTTCCAGCAATGATGAGCCAAATCTACATGAAGATG 681

RESULT 7
LOCUS BPE488589 875 bp mRNA linear PLN 05-MAR-2003
DEFINITION Betula pendula mRNA for PISTILLATA homologue (mads2 gene).
ACCESSION AJ488589
VERSION AJ488589.1 GI:28874429
KEYWORDS mads2 gene; PISTILLATA.
SOURCE Betula pendula (European white birch)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fagales; Betulaceae; Betula.

REFERENCE
1 Jarvinen, P., Lemmetyinen, J., Savolainen, O. and Sopanen, T.
AUTHORS DNA sequence variation in BpMADS2 gene in two populations of Betula
TITLE pendula
JOURNAL Mol. Ecol. 12 (2), 369-384 (2003)
MEDLINE 22423798
PubMed 12535088
REFERENCE
2 (bases 1 to 875)
AUTHORS Jaervinen, P. L. H.
Direct Submission
TITLE Submitted (29-MAY-2002) Jaervinen P. L. H., Biology, University of
JOURNAL Joensuu, P.O.Box 111, FIN-80101, Joensuu, FINLAND
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CDS
ORIGIN
Alignment Scores: 4.47e-52 Length: 875
Pred. No.:

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US-10-069-527-2 (1-215) x BPE488589 (1-875)

QY 1 MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20
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QY 21 TyrSerLysArgAspGlnGlyLysLysAlaLysGluIleThrValLeuCysAsp 40
Db 61 TACTCAAGAGGATGAAGGGGATCATAAAGAGGCTAAGGAGATCAGCAATCTTATGTGAT 120
QY 41 AlaLysValSerLeuIleLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 121 GCTAAAGTTCTCTTTGATCTTTGACAGCTCAGGAAAGATGAAGAGTACTGCACCT 180
QY 61 SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80
Db 181 TCAACTACGCTGATTAAACATCTTGGACATGTACCAAGCGGTCTGAGAAGAGATTGTGG 240
QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
Db 241 GATGCCAAATCAGAACCTCAGCAATGAATGCTAGATCAAGAAAGAGACGACAC 300
QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
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QY 121 LeuMetAlaLeuGlnGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
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Db 481 AATTTCATCTGCATCAGCAGCAGATGGCGATGGAAGCAGCAGCTGCAGAGACGTGGAA 540
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QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle 215
Db 589 GCTTTCCGCTGCAGCCTATTTCAGCAAAATCTACAAGATAGATG 633

RESULT 8
LOCUS NTGLOBOSA 768 bp mRNA linear PLN 10-JUN-1993
DEFINITION N. tabacum GLO mRNA.
ACCESSION X67959
VERSION X67959.1 GI:19870
KEYWORDS DNA binding protein; transcription factor.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 768)
AUTHORS Hansen, G., Estruch, J. J., Sommer, H. and Spena, A.
TITLE NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
Atirrhinum majus: cDNA sequence and expression pattern
JOURNAL Mol. Gen. Genet. 239 (1-2), 310-312 (1993)
MEDLINE 9328002
PubMed 8099711
REFERENCE
2 (bases 1 to 768)
AUTHORS Hansen, G.

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Qy	201	AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArg	214
Dd	:	:::: :::	
Dd	583	GCCTTCGGAGTTCAGCAATGCAGCCCTAAATTTCAGGAGAGA	624
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DEFINITION	Lilium regale LRGL0A mRNA for MADS-box transcription factor,		
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ACCESSION	AB071379		
VERSION	AB071379.1	GI:20513261	
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SOURCE	Lilium regale		
ORGANISM	Lilium regale		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;		
	Lilium.		
REFERENCE	1	Winter,K.U., Weiser,C., Kaufmann,K., Bohné,A., Kirchner,C., Kanno,A., Saedler,H. and Theissen,G. Evolution of class B floral homeotic proteins: obligate heterodimerization originated from homodimerization Mol. Biol. Evol. 19 (5), 587-596 (2002)	
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED	21959322		
REFERENCE	1	11961093	
AUTHORS	Kanno,A., Bohné,A., Saedler,H. and Theissen,G.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi 980-8577, Japan (E-mail:kanno@ge.tohoku.ac.jp, Tel:81-22-217-5725(ex.5725) Fax:81-22-217-5725)		

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ORIGIN
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DB:              8      Gaps:      3
US-10-069-527-2 (1-215) x AB071379 (1-822)
Qy      1 MetClyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgInValThr 20
Db      14 ATGGCGCGGGCAAGATCGAGATCAAGCGGATCGAGACTCGACCAATCGCCAGGTCACC 73
Qy      21 TyrSetLysArgArgAsnGlyIleIleLysLysAlaLysGluIleThrValLeuCysAsp 40

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Db, 74 TTCTCCAAGCGCCGCAACGGCATCATCAAGAAAGCCCGTGAGATCAGCGTCTCTGTGAG 133

QY 41 AlaLysValSerLeuIleTyrSerSerGlyLysMetValGluTyrCysSerPro 60
 DB 134 GCCAGGTCCTCGTCATCTCTCCAGCTCTGCAAGATGTCGAGTACTGCGAGCCCC 193

QY 61 SerThrThrLeuThrGluLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTyr 80
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QY 81 AspAlaLysHisGluLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
 DB 254 GATCCCAAGCATGAGCACCTGAGCGCGGAGATTGATGATCAAGAAGAGAGATGATA 313

QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 DB 314 ATGCATCCAGTCGAGGATCTGAAGGAGAGGATCTGAATCTGCTGCGCCGAGAGAG 373

QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
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QY 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
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QY 161 ThrTyrGluLeuGlnLysGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
 DB 494 ACTTATATCTGACCATCAGCAA---CTGGCAATGGATGAATATGAGGAACCTGGAA 550

QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPhe 200
 DB 551 TTGTCATATCATATAAGAT---GGGATTTTCAGTTCC-----CAGATGCCAATG 598

QY 201 AlaPheArgValGlnProLysGlnProAsnLeuGlnGlu 213
 DB 599 GCCTTCGTGTGAGCAATCCAGCCTAATTACATGAG 637

RESULT 10
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 LOCUS Hydrangea macrophylla MADS box containing protein PI mRNA, partial cds
 DEFINITION
 ACCESSION AF230711.1 GI:8163963
 VERSION
 KEYWORDS Hydrangea macrophylla
 ORGANISM Hydrangea macrophylla
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Cornales; Hydrangeaceae; Hydrangea.

REFERENCE 1 (bases 1 to 761)
 Krammer, E.M. and Irish, V.F.
 Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
 Int. J. Plant Sci. (2000) In press

REFERENCE 2 (bases 1 to 761)
 Krammer, E.M. and Irish, V.F.
 Direct Submission
 Submitted (03-FEB-2000) MCDB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA

FEATURES
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CDS

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ORIGIN

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 Query Match: 8 Gaps: 4
 DB:

US-10-069-527-2 (1-215) x AF230711 (1-761)

QY 26 AsnGlyIleLeuLysLysAlaLysGluIleThrValLeuCysAspAlaLysValSerLeu 45
 DB 1 AATGGGATCTTGAAGAGGCTAAGGAGATCCTGTTCTGTGTGATGCTAGTGTCTCTC 60

QY 46 IleIleTyrSerSerGlyLysMetValGluTyrCysSerProSerThrThrLeuThr 65
 DB 61 ATTGCTTTCTAGCTCTGCAAGATGCTAGTACTGTAGCCCCCAAAACCACTTGATT 120

QY 66 GluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuThrAspAlaLysHisGlu 85
 DB 121 GACATATTACAAATATATCATCTCAGTCTGGAAGAGGTTGTGGGATGCTAAGCATGAG 180

QY 86 AsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeu 105
 DB 181 AATCTAGCAATGAATTTGATAGATCAAGAAAGAGACGATAACATGCAGATTGAGCTA 240

QY 106 ArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGluLeuMetAlaLeuGlu 125
 DB 241 AGGCACCTGAAGGGGGAAGATGTACATCTTTGAACCAAGAGATCATGGCTTTGGAG 300

QY 126 GluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSerLysPheValAspMet 145
 DB 301 CTAGCCCTTGAGAAATGGCTTGTAGTATTCTGTCAGAAAGAGATGAGTCTTCGAGATG 360

QY 146 MetArgAspAsnGlyLys-----AlaLeuGluAspGluAsnLysArgLeuThrTyrGlu 163
 DB 361 ATTAAGAAATAATGTGAAATAATCAAGCACTTGAGGATGACAAAGCGCCCTTATTACGAG 420

QY 164 LeuGlnLysGlnGluMetLysIleLysGluAsnValArgAsnMetGluAsnGlyTyr 183
 DB 421 TTGCAC---CAGCAAGAGATGAATATGGATGGATGCAATGTAGAGAAATGGNAATGGGTAT 477

QY 184 HisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPheAlaPheArg 203
 DB 478 -----CAAAGGGTGGGAGACTACCACTCTCAT-----CAGATGGCTTTTGGCTTCAGG 525

QY 204 ValGlnProLysGlnProAsnLeuGlnGluArgIle 215
 DB 526 GTGCAGCAATTCAGCCAACTTACAGGAGAGAAATG 561

RESULT 11
 AB079259 807 bp mRNA linear PLN 02-APR-2003
 LOCUS Agapanthus praecox ApMADS1 mRNA for MADS-box transcription factor PI, complete cds.
 DEFINITION
 ACCESSION AB079259
 VERSION
 KEYWORDS AB079259.1 GI:29467045
 SOURCE Agapanthus praecox
 ORGANISM Agapanthus praecox
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Agapanthaceae; Agapanthus.

REFERENCE 1
 Nakamura, T. and Nakano, M.
 The MADS-box gene which expressed in floral organs of Agapanthus praecox
 Published Only in Database (2003)

Cy 181 AsnGlyTyrHisGlnArginLeuGlyAsnTyraSnAsnGlnGInGInleProPhe 200
|||:::
Db 578 CTCGGATATACCAGACAGAA-----AGGCAGTTTGCGGCCGAGATCCCAATG 625

Cy 201 AlaPheArgValGlnProIleGlnProAsnLeuCInGlu 213
|||||
Db 626 GCCTTCGCGGTGACGCCAATCCACCCAATTATCAGCAG 664

RESULT 12
ABO94967 876 bp mRNA linear PLN 31-OCT-2003
LOCUS Tulipa gesneriana TGGLO mRNA for MADS-box transcription factor,
complete cds.
ACCESSION ABO94967
VERSION AB094967.1 GI:30172224
KEYWORDS .
SOURCE Tulipa gesneriana
ORGANISM Tulipa gesneriana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Tulipa.

REFERENCE 1
AUTHORS Kanno,A., Saeki,H., Kameya,T., Siedler,H. and Theissen,G.
TITLE Heterotopic expression of class B floral homeotic genes supports a
modified ABC model for tulip (*Tulipa gesneriana*)
JOURNAL Plant Mol. Biol. 52 (4), 831-841 (2003)
MEDLINE 22856392
PubMed 13677470
REFERENCE 2 (bases 1 to 876)
Kanno,A.
Direct Submission
Submitted (28-OCT-2002) Akita Kanno, Tohoku University, Graduate
School of Life Sciences; Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail:kanno@ise.tohoku.ac.jp, Tel:81-22-217-5725,
Fax:81-22-217-5725)

FEATURES
source location/Qualifiers
 1..876
 /organism="Tulipa gesneriana"
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 /db_xref="taxon:13306"
 /tissue_type="flower"
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 /gene="TGGLO"
CDs 20..655
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product="MADS-box transcription factor"
protein_id="BAC75972.1"
db_xref="GI:30172225"
translations="MGRIKEIKRINSTNRQVTFSKRNRIGKKAREISVLCDAWYS
VFUDDSKNGSEYCSPTITPKMLDQQCNGLWDAXHNLSEEIDRKKNNDNQW
IEURHLKGDLNLSQKELIPIEALENGPSVRKODDVLMTRKKMRIMLEEDNKKL
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ORIGIN

Alignment Scores:
Pred. No.: 4,75e-50 Length: 876
Score: 696.00 Matches: 131
Percent Similarity: 77.93% Conservative: 35
Best Local Similarity: 61.50% Mismatches: 43
Query Match: 63.10% Indels: 4
DB: 8 Gaps: 1

US-10-069-527-2 (1-215) x ABO94967 (1-876)

Cy 1 MercGlyArgGlyLysValGlulleLysArqileGluasnsSerAsnArgInvalThr 20
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Db 20 ATGGCGCGCGGAAGATCGAAATCAAGCGCATCGAAGCTCCACCAACCCCAGTCACC 79

Cy 21 TyrserLyssArgAsnGngyllelleLysAlalysGllulleThrValLeuCysAsp 40
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Db		80	TTCCTCCAGCGCCGCAACGGGATCATCAAGAAGCGGAGGAGATCAGCTGTCTGGCAC	139
QY		41	AlaLysValSerLeullelleTyTrSerSerGlyLysMetValGluTyrCysSerPro	60
Db		140	GCTGGGTCTCTGTCGTATATTCTCCAGCTCCGGGAAGATGCCGAGTACTGCAGCCCC	199
QY		61	SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyClnSerGlyLysLysLeuTrp	80
Db		200	ACCATCATCGCTACCGAAGATCTCGACAAGTACACGAGAACTGCCGGGAACAAGTCTTGG	259
QY		81	AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysLysAspAsnSper	100
Db		260	GAGCGCAGCACCCAGATCTGAGCGAGAGATTGATAGGATCAGAAGGAGAACGACAC	319
QY		101	MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu	120
Db		320	ATGCAGATAGAGCTGAGGCATCTCAAGGGGAGAGTCTGAACCTCGCTGCAGCCCAGGAG	379
QY		121	LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer	140
Db		380	CTGATCCCGATTGAGAGCGCTCGAGACCGTTTCAGGAGCGTGAGGAGGAGCAGGAT	439
QY		141	LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu	160
Db		440	GATGTGCTGATGACGAGGAAGAATAATGATGAGCTGATGAGGAGGATTAACAAACGGCTG	499
QY		161	ThrTyrGluLeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGlu	180
Db		500	AATATGTACTGTCATCACACACACACAGCAATGATGAAAATATATAGGAGCATGGAG	559
QY		181	AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIlePropHe	200
Db		560	CTTGCTATCATCAGAAA-----CATAGGGAATTCAATTCCAGATGCCAATG	607
QY		201	AlaPheArgValGlnProIleGlnProAsnLeuGlnGlu	213
Db		608	ACGTTCCGTGTGAGCCCAATTACGCTAATTGTCATGAG	646
RESULT 13				
GHV9726				
LOCUS				
DEFINITION			GHV9726 Gerbera hybrida cv. 'Terra Regina' mRNA for MADS-box protein, GGLO1.	
ACCESSION			AJ009726	
VERSION			AJ009726.1 GI:4218172	
KEYWORDS			ggl1 gene; MADS-box protein.	
SOURCE			Gerbera hybrid cv. 'Terra Regina'	
ORGANISM			Gerbera hybrid cv. 'Terra Regina' Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Mutisioideae; Mutisiae; Gerbera.	
REFERENCE			1 Yu.D., Korilainen,M., Pollanen,E., Mehto,M., Elomaa,P., Helariutta,Y., Albert,V.A. and Teeri,T.H. Organ identity genes and modified patterns of flower development in Gerbera hybrida (Asteraceae) Plant J. 17 (1), 51-62 (1999)	
JOURNAL			2 (bases 1 to 810)	
MEDLINE			Teeri,T.H.	
PUBMED			Direct Submission	
REFERENCES			Submitted (21-JUL-1998) Teeri T.H., Institute of Biotechnology, University of Helsinki, P.O. Box 56, FIN-00014 Univ. Helsinki,	
JOURNALS			FINLAND	
FEATURES			Location/Qualifiers	
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			/mol_type="mRNA"	
			/cultivar="Terra Regina"	
			/db_xref="taxon:226891"	
gene			1..810	

LOCUS AY173061 814 bp mRNA linear PLN 20-JAN-2003
DEFINITION Chrysanthemum x morifolium MADS-box transcription factor CDM86
ACCESSION AY173061
VERSION AY173061.1 GI:27804368
KEYWORDS Chrysanthemum x morifolium (Dendrathera grandiflora)
SOURCE Chrysanthemum x morifolium
ORGANISM Chrysanthemum x morifolium
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Anthemideae; Chrysanthemum.
REFERENCE 1 (bases 1 to 814)
AUTHORS Shchennikova, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
TITLE Chrysanthemum MADS-box transcription factor CDM86
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 814)
AUTHORS Shchennikova, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2002) Plant Development and Reproduction, Plant
Research International, Droevendaalsesteeg 1, Wageningen 6700 AA,
The Netherlands
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source
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Location/Qualifiers
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/mol_type="mRNA"
/culturvar="Parliament"
/db_xref="taxon:41568"
/tissue_type="inflorescence"
/notes="synonym: Dendrathera grandiflora"
1. .814
/genes="cdm86"
37. .627
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/notes="APETALA3/PISTILLATA subfamily; similar to
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/codon_start=1
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/protein_id="AA022986.1"
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MYLVOOSEAAAGDYOAEFFPFRVQPMQPNLHERN"
ORIGIN
Alignment Scores:
Pred. No.: 3 36e-49 Length: 814
Score: 685.50 Matches: 136
Percent Similarity: 76.28% Conservative: 28
Best Local Similarity: 63.26% Mismatches: 32
Query Match: 62.15% Indels: 19
DB: 8 Gaps: 3
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QY 1 MetGlyArgGlyLysValGluLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 37 ATGGCGCAGGGAAGATAGAGATCAAGAGATAGAAAACACAGTAACAGCAAGTCACA 96
QY 21 TyrSerLysArgArgAsnGlyLysLysLysLysLysLysLysLysLysLysLysLys 40
Db 97 TATTCAAAAGAAGAAGATGGATCATCAAGAAAGCTAAGAAATATACTGTTCTTGAT 156
QY 41 AlalysValSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db 157 GCTAATGTCCTCTTGTATCTATCTGATCTCTTCGCAAGATGATGAGTACTGCAGCCCT 216
QY 61 SerThrThrThrGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 80
Db 217 AAAAATAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 276
QY 81 AspAlalysHisGluAsnLeuSerAsnGluValAspArgValLysLysLysAspSer 100

Db 277 GATCTAAACATGAGATCTTCAGAAATGATAGAAATCAAGAAAGAAATGAAGC 336
QY 101 MetGlnValGluLeuArgHisLeuLysGlyGlyLysLysLysLysLysLysLysLys 120
Db 337 ATGCAATAGAGCTCAGGCACCTTCAGGGAAGATATACATCTTTGAACATGAAGAA 396
QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerLysArgAspLysGlnSer 140
Db 397 CTAATTCGGTATGAAGATGCACCTTGAAGATGCACCTTGAAGATGCACCTTGAAGAT 456
QY 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
Db 457 GACATCCCAAAATCATGAGGAACATGAGCAAGCTTTGGAGGAGGAAATAAGCATCTT 516
QY 161 ThrTyrGluLeuGlnLysGlnGlnGluMetLysLysLysLysLysLysLysLysLys 180
Db 517 ATGTAT---TTAGTGCACCAAGTGAATG-----CAAGCTCATGAGACCTTT 543
QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnGlnGlnGln 200
Db 544 -----GCAGCATGGAGATAC-----CAAGCTCATGAGACCTTT 579
QY 201 AlaPheArgValGlnProGlnProAsnLeuGlnGluArgIle 215
Db 580 TCATTTGTCAGCAATGCAGCTTAACCTGATGAGAGATG 624
RESULT 15
LOCUS A36587 780 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent WO9400582.
ACCESSION A36587
VERSION A36587.1 GI:2293891
KEYWORDS Petunia x hybrida
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.
REFERENCE 1 (bases 1 to 780)
AUTHORS Van, T.A., Mollema, C., Angenent, G.C. and Dons, J.J.
TITLE A METHOD FOR OBTAINING A PLANT HAVING ALTERED FLORAL MORPHOLOGY AND
A METHOD FOR PROTECTING PLANTS AGAINST PEST INSECTS
JOURNAL Patent: WO 9400582-A 1 06-JAN-1994;
FOR PLANT BREEDING AND REPRODU (NL)
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1. .780
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8. .640
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ORIGIN
Alignment Scores:
Pred. No.: 3 89e-49 Length: 780
Score: 684.50 Matches: 134
Percent Similarity: 82.33% Conservative: 43
Best Local Similarity: 62.33% Mismatches: 33

Query Match:	62.06%	Indels:	5
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US-10-069-527-2 (1-215) x A36587 (1-780)			
Qy	1	MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr	20
Db	8	ATGGGAGAGGAAGATAGATAGATAAAAGATAGAAACTCAGCAACAGACAAGTAAC	67
Qy	21	TyrSerLysArgArgAsnGlyIleIleLysLysAlaLysGluIleThrValLeuCysAsp	40
Db	68	TACTCAAAAGAGAAATCGGATCTTGAATAAAGCTAAGGAAATTAGTGTTCTTGTGAT	127
Qy	41	AlaLysValSerLeuIleIleTyrSerSerGlyLysMetValGluTyrCysSerPro	60
Db	128	GCTCGTGTTCGTGTTATCATTTTGTAGCTCTGGCAAGATGCATGAGTTC-----TCT	181
Qy	61	SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuThr	80
Db	182	TCCTACTCGTGTGGTGGATTTTGATCAATATCACAAAGCTTACTGCTAGAAAGTTGTTG	241
Qy	81	AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer	100
Db	242	GATGCTAAGCATGAGAACTTGACAAATCAAAAGTCAAGAAAGACAATGACAAC	301
Qy	101	MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu	120
Db	302	ATGCAAAATTGAATCAGGCACCTTGAGGGGTGAAGATATCATCTTTGAAACCATAGAGAG	361
Qy	121	LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer	140
Db	362	CTCATGATATTGGAAGATGCCCTTGAAATATGGACTCACTAGTATTGTAACAAACAGAA	421
Qy	141	LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu	160
Db	422	GAGTTTCTGAGGATGATGAGGAAAAGACTCAAAATGTGAGGAGGAGCAAGACCAACTT	481
Qy	161	ThrTyrGluLeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGlu	180
Db	482	AATTGGCAATTGGCCAACTTGAGATGCAACCATGAATAGGAATATGGGAGAAATTGGC	541
Qy	181	AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAspAsnGlnGlnIleProPhe	200
Db	542	GAACTGTTTCAGCAGAGGGGAATCATCATGATACCAAAACCAT-----ATGCCTTTT	592
Qy	201	AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle	215
Db	593	GCCTTCCGAGTACAACTTATGAGCAAAATTTGAGGAGAGGTTG	637

Search completed: September 26, 2004, 09:11:12
Job time : 3677.24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:18:34 ; Search time 69.2617 Seconds
(without alignments)
979.421 Million cell updates/sec

Title: US-10-069-527-2
Perfect score: 1103
Sequence: 1 MGSKVEIKRIENSNRQVT.....QQIPFAFRVQIOPNLQERI 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:
1: sp archaea:
2: sp bacteria:
3: sp fungi:
4: sp human:
5: sp invertebrate:
6: sp mammal:
7: sp mhc:
8: sp organelle:
9: sp phage:
10: sp plant:
11: sp rodent:
12: sp virus:
13: sp vertebrate:
14: sp unclassified:
15: sp rvirus:
16: sp bacteriap:
17: sp archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	215	10 Q9AVU7	Q9AVU7 malus domes
2	1099	99.6	215	10 Q9AVU6	Q9AVU6 malus domes
3	975	88.4	190	10 Q8LSM9	Q8LSM9 malus domes
4	824	74.7	211	10 Q9ZTQ9	Q9ZTQ9 cucumis sat
5	811	73.5	203	10 Q9FZNI	Q9FZNI rosa rugosa
6	739.5	67.0	212	10 Q40883	Q40883 petunia hyb
7	720	65.3	211	10 Q84110	Q84110 betula verr
8	701.5	63.6	210	10 Q8LT09	Q8LT09 lilium rega
9	698.5	63.3	187	10 Q9LL94	Q9LL94 hydrangea m
10	698.5	63.3	210	10 Q84L87	Q84L87 agapanthus
11	696	63.1	211	10 Q84W20	Q84W20 tulipa gesn
12	691	62.6	197	10 Q9ZS26	Q9ZS26 gerbera hyb
13	685.5	62.1	196	10 Q84LC9	Q84LC9 chrysanthem
14	684	62.0	213	10 Q41353	Q41353 silene lati
15	669.5	60.7	208	10 Q64934	Q64934 eucalyptus
16	666	60.4	202	10 Q9XF83	Q9XF83 hyacinthus

17	664	60.2	209	10 Q8GTP3	Q8GTP3 orchis ital
18	664	60.2	229	10 Q65124	Q65124 dicentra ex
19	663.5	60.2	200	10 Q9LL95	Q9LL95 chloranthus
20	663.5	60.2	208	10 Q9SEF9	Q9SEF9 arabidopsis
21	660.5	59.9	196	10 Q84LC2	Q84LC2 helianthus
22	647	58.7	196	10 Q65129	Q65129 delphinium
23	642.5	58.3	212	10 Q9AR49	Q9AR49 zea mays (m
24	641.5	58.2	212	10 Q9AR50	Q9AR50 zea mays (m
25	638	57.8	202	10 Q9XF84	Q9XF84 hyacinthus
26	633	57.4	186	10 Q9LL97	Q9LL97 calycanthus
27	633	57.4	216	10 Q8LSF6	Q8LSF6 daucus caro
28	625	56.7	186	10 Q65130	Q65130 michelia fi
29	623	56.5	209	10 Q9AR51	Q9AR51 zea mays (m
30	620.5	56.3	210	10 Q40703	Q40703 oryza sativ
31	618.5	56.1	187	10 Q84V60	Q84V60 cimicifuga
32	617	55.9	209	10 Q40702	Q40702 oryza sativ
33	615.5	55.8	185	10 Q65131	Q65131 liriodendro
34	611.5	55.4	212	10 Q94FT9	Q94FT9 medicago sa
35	609	55.2	200	10 Q65128	Q65128 syringa vul
36	608.5	55.2	186	10 Q9LL92	Q9LL92 tacca chant
37	608.5	55.2	187	10 Q84V89	Q84V89 akebia quin
38	607.5	55.1	187	10 Q84V59	Q84V59 cimicifuga
39	606	54.9	231	10 Q65122	Q65122 papaver nud
40	605.5	54.9	187	10 Q84V88	Q84V88 akebia quin
41	597.5	54.2	185	10 Q84V64	Q84V64 berberis gi
42	596.5	54.1	208	10 Q9LL93	Q9LL93 sagittaria
43	595	53.9	167	10 Q8GT92	Q8GT92 helianthus
44	593.5	53.8	170	10 Q84Y29	Q84Y29 trolius la
45	593.5	53.8	181	10 Q8LT08	Q8LT08 lilium rega

ALIGNMENTS

RESULT 1

Q9AVU7 PRELIMINARY; PRT; 215 AA.
ID Q9AVU7
AC Q9AVU7
DT 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DE 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Pistillata MADS-box protein.
GN PI.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Granny Smith; TISSUE=Flower;
RX MEDLINE=21107711; PubMed=11158635;
RA Yao J.L., Dong Y.H., Morris B.A.;
RT "Parthenocarpic apple fruit production conferred by transposon
RT insertion mutations in a MADS-box transcription factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1306-1311(2001).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
CC EMBL; AJ291490; CAC28021.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T05238; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.

DR PROSITE; PS00066; MADS BOX 2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 215 AA; 24999 MW; 51F6E2B849ADB26C CRC64;

Query Match 100.0%; Score 1103; DB 10; Length 215;
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60
 Db
 QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60
 Db
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120
 Db
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120
 Db
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALDENKRLTYELQKQEMKIKENVRNME 180
 Db
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALDENKRLTYELQKQEMKIKENVRNME 180
 Db
 QY 181 NGYHQRLGNYNQOQIPPAFRVQPIQPNLQERI 215
 Db
 QY 181 NGYHQRLGNYNQOQIPPAFRVQPIQPNLQERI 215
 Db

RESULT 2
 Q9AVU6 PRELIMINARY; PRT; 215 AA.
 ID Q9AVU6
 AC Q9AVU6
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Placillata MADS-box protein.
 GN PI.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Granny Smith; TISSUE=Leaf;
 RX MEDLINE=21107711; PubMed=1158635;
 YAO J.L., Dong Y.H., Morris B.A.;
 RT "Parthenocarpic apple fruit production conferred by transposon
 insertion mutations in a MADS-box transcription factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1306-1311(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AJ291491; CAC28022.1; -.
 DR HSSP; P11746; 1MNW.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 215 AA; 25000 MW; 51F6E2B849ADB26C CRC64;

Query Match 99.6%; Score 1099; DB 10; Length 215;
 Best Local Similarity 99.5%; Pred. No. 1.4e-63;
 Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60
 Db

Db
 QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120
 Db
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120
 Db
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALDENKRLTYELQKQEMKIKENVRNME 180
 Db
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALDENKRLTYELQKQEMKIKENVRNME 180
 Db
 QY 181 NGYHQRLGNYNQOQIPPAFRVQPIQPNLQERI 215
 Db
 QY 181 NGYHQRLGNYNQOQIPPAFRVQPIQPNLQERI 215
 Db

RESULT 3
 Q8LSM9 PRELIMINARY; PRT; 190 AA.
 ID Q8LSM9
 AC Q8LSM9
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE MADS-box protein (Fragment).
 GN MDPI.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indo; TISSUE=Young floral parts;
 RA Matsumoto S., Ohtsubo T., Soejima J.;
 RT "Cloning and sequencing of apple MADS-box genes 'MdPI', 'MdTM6' and
 'MdMADS13'.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AB081092; BAC11906.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 FT NON TER 1
 SQ SEQUENCE 190 AA; 22025 MW; 9D6ED732D01B5D9 CRC64;

Query Match 88.4%; Score 975; DB 10; Length 190;
 Best Local Similarity 99.5%; Pred. No. 1.2e-55;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 26 NGIHKAKEITVLCDKAVSLIIYSSSGKMWVCSPSTTLTEILDYKHGSGKKLWDKAKEH 85
 Db
 QY 1 NGIHKAKEITVLCDKAVSLIIYSSSGKMWVCSPSTTLTEILDYKHGSGKKLWDKAKEH 85
 Db
 QY 86 NLSNEVDYKNDNSMQVELRHLKGEDITSLNHVELMALEAEALENGLTSIRDKQSKFVDM 145
 Db
 QY 61 NLSNEVDYKNDNSMQVELRHLKGEDITSLNHVELMALEAEALENGLTSIRDKQSKFVDM 120
 Db
 QY 146 MRDNGKALDENKRLTYELQKQEMKIKENVRNMGYHQRLGNYNQOQIPPAFRVQ 205
 Db
 QY 121 MRDNGKALDENKRLTYELQKQEMKIKENVRNMGYHQRLGNYNQOQIPPAFRVQ 180
 QY 206 PIQPNLQERI 215
 Db
 QY 181 PIQPNLQERI 190

RESULT 4
Q92TQ9 PRELIMINARY; PRT; 211 AA.
ID Q92TQ9
AC Q92TQ9
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MADS-box protein 26.
GN CUM26.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OC NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RA Kater M.M., Franken J., Carney K., van Lookeren Campagne M.M.,
Angelier G.C.;
RT "class C homeotic genes are required for whorl specific sex
determination in unisexual flowers";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
DR EMBL: AF043255; AAD02250.1; -.
DR HSSP: P11746; 1NMN.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 211 AA; 24904 MW; D89FD0B1A979C03 CRC64;

Query Match 74.7%; Score 824; DB 10; Length 211;
Best Local Similarity 73.8%; Pred. No. 7.5e-46;
Matches 158; Conservative 34; Mismatches 18; Indels 4; Gaps 2;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKAKEITVLCDAKVSIIITSSSGKWEYCSG 60
DB 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKAKEITVLCDAKVSIIITSSSGKWEYCSG 60
QY 61 STLTLEILDYKHGSGKKLWDAKHENLSNEVDYKNDMSQVLELRKLGEDITSINHV 120
DB 61 STLTLEILDYKHGSGKKLWDAKHENLSNEVDYKNDMSQVLELRKLGEDITSINHV 120
QY 121 LMALEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 180
DB 121 LMALEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 180
QY 121 LMALEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 180
DB 121 LMALEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 180
QY 181 NGYHQRQLGYNVNNQOQIPFAFRVQPIQPLQER 214
DB 181 NGYHQRQLGYNVNNQOQIPFAFRVQPIQPLQER 214
QY 181 IGYNQR-MRDPNS---QMPFAFRVQPIQPLQER 210
DB 181 IGYNQR-MRDPNS---QMPFAFRVQPIQPLQER 210

RESULT 5
Q9FZNI PRELIMINARY; PRT; 203 AA.
ID Q9FZNI
AC Q9FZNI
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MADS-box protein.
GN MASAKO BP.

OS Rosa rugosa (Rugosa rose).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OC NCBI_TaxID=74645;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Flower.
RA Matsumoto S., Kitahara K., Hirai S., Wada K., Fukui H.;
RT "Rose MADS-box gene 'MASAKO' BP homologous to class B floral identity
genes";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
DR EMBL: AB038462; BAB11939.1; -.
DR HSSP: P11746; 1NMN.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 203 AA; 23573 MW; C577C9A497FBEDC CRC64;

Query Match 73.5%; Score 811; DB 10; Length 203;
Best Local Similarity 75.0%; Pred. No. 4.9e-45;
Matches 162; Conservative 20; Mismatches 20; Indels 14; Gaps 4;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKAKEITVLCDAKVSIIITSSSGKWEYCSG 59
DB 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKAKEITVLCDAKVSIIITSSSGKWEYCSG 60
QY 60 PSTLTLEILDYKHGSGKKLWDAKHENLSNEVDYKNDMSQVLELRKLGEDITSINHV 119
DB 60 PSTLTLEILDYKHGSGKKLWDAKHENLSNEVDYKNDMSQVLELRKLGEDITSINHV 120
QY 120 ELMLEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 179
DB 120 ELMLEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 179
QY 121 DLMLEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 178
DB 121 DLMLEELNGLTISIRKQSKPVDMDKNGKALDENKRLTYLQKQEKIKENRANE 178
QY 180 ENGYHQRQLGYNVNNQOQIPFAFRVQPIQPLQER 215
DB 180 ENGYHQRQLGYNVNNQOQIPFAFRVQPIQPLQER 215
QY 179 -----NYYNN-TQIPFALRVQNPQNLHDM 203
DB 179 -----NYYNN-TQIPFALRVQNPQNLHDM 203

RESULT 6
Q40883 PRELIMINARY; PRT; 212 AA.
ID Q40883
AC Q40883
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FBP3.
GN FBP3.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Petunia.
OC NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=R27; TISSUE=Petal;
RA MEDLINE=94177174; PubMed=7907515;
RA Angelier G.C., Franken J., Buscher M., Weiss D., van Tuinen A.V.;
RT "Co-suppression of the Petunia homeotic gene fbp2 affects the identity

RT of the generative meristem."
 RL Plant J 5:33-44(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL: X71417; CAA50549.1; -.
 DR PIR: S60288; S60288.
 DR HSSP: P11746; 1MMN.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO: GO:0006350; P:transcription; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS0066; MADS_BOX_2; 1.
 KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 212 AA; 24740 MW; 712351a6c8369f CRC64;
 Query Match 67.0%; Score 739.5; DB 10; Length 212;
 Best Local Similarity 67.4%; Pred. No. 2.1e-40;
 Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60
 QY 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 DB 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 DB 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 DB 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 QY 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 DB 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 QY 181 NGYHQRGLGNVNNQOQIPPAFRVOPIDPNOER1 215
 DB 181 NGYHQRGLGNVNNQOQIPPAFRVOPIDPNOER1 215
 DB 181 EYVHQR---DRDYEQQWFFALRVQPMQPNLHERM 212
 RESULT 7
 Q84L10 PRELIMINARY; PRT; 211 AA.
 AC Q84L10;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Pistillata homologue.
 OS Betula verrucosa (White birch) (Betula pendula).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosida I; Fagales; Betulaceae; Betula.
 OC NCBI_TaxID=3505;
 RN NCBI_TaxID=3505;
 RN SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RA Jaervinen P.L.H., Lemmetyinen J., Savolainen O., Sopanen T.;
 RT "DNA sequence variation in Bpmads2 gene in two populations of Betula
 RT pendula.";
 RT Mol. Ecol. 12:369-384 (2003).
 DR EMBL: A0486589; CAD32764.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.

DR PRINTS: PR00404; MADSOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS0066; MADS_BOX_2; 1.
 SQ SEQUENCE 211 AA; 24930 MW; F9B96C504C1E26DC CRC64;
 Query Match 65.3%; Score 720; DB 10; Length 211;
 Best Local Similarity 66.0%; Pred. No. 3.8e-39;
 Matches 142; Conservative 31; Mismatches 38; Indels 4; Gaps 2;
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60
 QY 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 DB 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 DB 61 STTLEILDKYHGQSGKMLDAKHENLSNEVDVRKKNDSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 DB 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 DB 121 LMALEALENGSLTIRDKQSKFVDMWRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
 QY 181 NGYHQRGLGNVNNQOQIPPAFRVOPIDPNOER1 215
 DB 181 NGYHQRGLGNVNNQOQIPPAFRVOPIDPNOER1 215
 DB 181 DYVHQR---DRDYEQQWFFALRVQPMQPNLHERM 211
 RESULT 8
 Q8LTO9 PRELIMINARY; PRT; 210 AA.
 AC Q8LTO9;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE MADS-box transcription factor.
 GN LRGLOA.
 OS Lilium regale (Regal lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OC NCBI_TaxID=82328;
 RN NCBI_TaxID=82328;
 RN SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RA MEDLINE=21955932; PubMed=11961093;
 RA Winter K.U., Weiser C., Kaufmann K., Bohne A., Kirchner C., Kanno A.,
 RA Saedler H., Theissen G.;
 RT "Evolution of Class B Floral Homeotic Proteins: Obligate
 RT Heterodimerization Originated from Homodimerization.";
 RT Mol. Biol. Evol. 19:587-596(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL: AB071379; BAB91551.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO: GO:0006350; P:transcription; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS0066; MADS_BOX_2; 1.
 KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 210 AA; 24621 MW; F2F3262F364EEB4E CRC64;
 Query Match 63.6%; Score 701.5; DB 10; Length 210;
 Best Local Similarity 62.0%; Pred. No. 6e-38;
 Matches 122; Conservative 45; Mismatches 31; Indels 5; Gaps 3;
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKKAKETITVLCDAKVSLLIYSSGGMVEYCSF 60

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Db 1 MGRGKIEIKRIENSTNRQVTFPSKRRNGIIRKAREISVLCEAQSIVIFSSGKMSYVCSF 60
QY 61 STLTLEILLDKYHGSGKRLMDAKHENLSNEVDYRKDNDQVLELRLHKGEDITSLNHVE 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 STSLPRLIERVQYNGCGKIMDPGRHEHLSAIDRIKKENDNMQILRLHKGEDLNSLDQPE 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 LMALEBALENGSLTIRDKOSKFPVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 LIPIEBALENGSLGVAREKQNDFLRLMKKERRILEENKRLTYILRHQ-LAMDENNRNL 179
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 NGYHQRQLGNTNNNQOQIPPAFRVQPIQPILOE 213
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 FAYHND-GDFSS---QMPMAFRVQPIQPILOE 208
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
Q9LL94 PRELIMINARY; PRT; 187 AA.
ID Q9LL94
AC Q9LL94;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MADS box containing protein PI (Fragment).
OS Hydrangea macrophylla.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Cornales; Hydrangeaceae; Hydrangea.
OX NCBI_Taxid=31110;
RN [1]
RP SEQUENCE FROM N.A.
RA Kramer E.M., Irish V.F.;
RT Evolution of the petal and stamen developmental programs: Evidence
RT from comparative studies of the lower eudicots and basal
RT angiosperms.
RT Int. J. Plant Sci. 0:0-0(2000).
CC - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC - FACTORS.
DR EMBL; AF230711; AAF73940.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.
FT NDN_TER 1
SQ SQUENCE 187 AA; 21844 MW; C7CE02871F635034 CRC64;

Query Match 63.3%; Score 698.5; DB 10; Length 187;
Best Local Similarity 71.4%; Pred. No. 8.2e-38;
Matches 137; Conservative 29; Mismatches 19; Indels 7; Gaps 4;

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RESULT 10
Q84L87 PRELIMINARY; PRT; 210 AA.
ID Q84L87
AC Q84L87;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MADS-box transcription factor PI.
GN APMAD51.
OS Agapanthus praecox.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Agapanthaceae;
OC Agapanthus.
OX NCBI_Taxid=186128;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Royal purple select; TISSUE=Floral bud;
RA Nakamura T., Nakano M.;
RT "The MADS-box gene which expressed in floral organs of Agapanthus
RT praecox."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB079259; BAC66962.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TE; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 210 AA; 24656 MW; 397E143EE3013A1C CRC64;

Query Match 63.3%; Score 698.5; DB 10; Length 210;
Best Local Similarity 62.0%; Pred. No. 9.3e-38;
Matches 132; Conservative 41; Mismatches 35; Indels 5; Gaps 2;

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RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;
RT "Heterotopic expression of class B floral homeotic genes supports a
RT modified ABC model for tulip (Tulipa gesneriana).";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB094967; BAC75972.1; -;
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PRO0404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR SEQUENCE 211 AA; 25022 MW; A785CD6275573692 CRC64;

Query Match 63.1%; Score 696; DB 10; Length 211;
Best Local Similarity 61.5%; Pred. No. 1,4e-37;
Matches 131; Conservative 35; Mismatches 43; Indels 4; Gaps 1;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120
QY 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
DB 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
QY 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
DB 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
QY 181 NGYHOROGLNYYNNQOIPPAFRVOPIONLOE 213
DB 181 NGYHOROGLNYYNNQOIPPAFRVOPIONLOE 213
QY 181 LAHQK---HREPSQMPFRVOPIONLHE 209
DB 181 LAHQK---HREPSQMPFRVOPIONLHE 209

RESULT 12

Q9ZS26 PRELIMINARY; PRT; 197 AA.

AC 09ZS26; 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MADS-box protein, GLO1.
GN GLO1.
OS Gerbera hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asterales; Mutilisidaceae; Mutilisaceae; Gerbera.
OX NCBI_Taxid=18101;
RN [1] _SEQUENCE FROM N.A.
RC STRAIN=cy. Terra Regina;
RA MEDLINE=99168221; PubMed=10069667;
RA Yu D., Kotilainen M., Poellänen B., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RA "Organ identity genes and modified patterns of flower development in
RT Gerbera hybrida (Asteraceae).";
RL Plant J. 17:51-62(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL: AJ009726; CAA08804.1; -;
DR HSPF: P11746; INNM.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006355; P:transcription; IEA.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.

DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PRO0404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
DR SEQUENCE 197 AA; 23133 MW; DDDIC2B2E01C5A2A CRC64;

Query Match 62.8%; Score 691; DB 10; Length 197;
Best Local Similarity 63.3%; Pred. No. 2,6e-37;
Matches 136; Conservative 30; Mismatches 31; Indels 18; Gaps 3;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120
QY 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
DB 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
QY 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
DB 121 LMALBEALENGTLISIDKOSKFLVDMRDNGKALEDENRILTYELQKQEMKIKENYRME 180
QY 181 NGYHOROGLNYYNNQOIPPAFRVOPIONLOE 215
DB 181 NGYHOROGLNYYNNQOIPPAFRVOPIONLOE 215
QY 170 ----AAGDYQAHE--PFRVOPIONLHERM 197
DB 170 ----AAGDYQAHE--PFRVOPIONLHERM 197

RESULT 13

Q84LC9 PRELIMINARY; PRT; 196 AA.

AC 084LC9; 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MADS-box transcription factor CDM86.
GN CDM86.
OS Chrysanthemum x morifolium.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asterales; Anthemideae; Anthemideae;
OX Chrysanthemum.
OX NCBI_Taxid=41568;
RN [1] _SEQUENCE FROM N.A.
RC STRAIN=cy. Parliament; TISSUE=flower;
RA Shchemnikova A.V., Shulga O.A., Skryabin K.G., Angenent G.C.;
RT "Chrysanthemum MADS-box transcription factor CDM86.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY173061; AAC22986.1; -;
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PRO0404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR SEQUENCE 196 AA; 22593 MW; 84D0035B13E121D0 CRC64;

Query Match 62.1%; Score 685.5; DB 10; Length 196;
Best Local Similarity 63.3%; Pred. No. 6e-37;
Matches 136; Conservative 28; Mismatches 32; Indels 19; Gaps 3;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSSGKMYEYCS 60
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHILKGEDITSINHYE 120

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: September 27, 2004, 09:11:24 / Search time 14.4295 Seconds
(without alignments)
775.845 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103
Sequence: 1 MGRGVEIRIENSSNRQVT.....QQIPPAFVQPIQPLQERI 215

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740.5	67.1	212	1	MAD2_PETHY 007474 petunia hyb
2	713	64.6	215	1	GLOB_ANTMA 003378 antirrhinum
3	707	64.1	210	1	GLOB_TOBAC 003416 nicotiana t
4	684.5	62.1	210	1	FBP1_PETHY 003488 petunia hyb
5	660.5	59.9	208	1	PIST_PETHY 048007 arabidopsis
6	421	38.2	237	1	M13_GNEGN 09xj14 gnetum gnm
7	384.5	34.9	259	1	M17_MAZE 08vwm8 zea mays (m
8	377.5	34.2	231	1	MAD1_PETHY 007472 petunia hyb
9	373.5	33.9	247	1	DE21_ANTMA 08r114 antirrhinum
10	360.5	32.7	268	1	FB24_PETHY 09ates petunia hyb
11	356.5	32.3	222	1	AP3_ARATH 035632 arabidopsis
12	349	31.6	227	1	DEFA_ANTMA 08r106 antirrhinum
13	342	31.0	252	1	TTL6_ARATH 08r109 arabidopsis
14	335	30.4	251	1	SEB3_ARATH 02456 arabidopsis
15	334	30.3	265	1	JOIN_LYCES 09fiv6 lycopersico
16	332	30.1	214	1	CMB2_DIACA 042498 dianthus ca
17	330	29.9	242	1	AGL6_ARATH 038676 arabidopsis
18	329	29.8	254	1	AGL5_SINLA 004067 sinapis alb
19	327.5	29.7	251	1	SEB1_ARATH 029382 arabidopsis
20	326.5	29.6	258	1	AGL3_ARATH 029383 arabidopsis
21	323.5	29.3	250	1	AGL8_SOLTU 042429 solanum tub
22	322	29.2	241	1	AGL4_SINLA 041274 sinapis alb
23	322	29.2	253	1	CAL_ARATH 039081 arabidopsis
24	320.5	29.1	248	1	AGL1_ARATH 029381 arabidopsis
25	319.5	29.0	246	1	AGL5_ARATH 029385 arabidopsis
26	319	28.9	252	1	AG_ARATH 017839 arabidopsis
27	318.5	28.9	241	1	AGL9_PETHY 003495 petunia hyb
28	318	28.8	254	1	AP1_SINLA 041276 sinapis alb
29	318	28.8	256	1	AP1_ARATH 035631 arabidopsis
30	316	28.6	240	1	SVP_ARATH 09fvc1 arabidopsis
31	314.5	28.5	250	1	AGL8_SOLCO 022328 solanum com
32	314	28.5	250	1	SEB2_ARATH 029384 arabidopsis
33	313	28.4	227	1	AGL6_LYCES 040170 lycopersico

ALIGNMENTS

RESULT 1	MAD2_PETHY	STANDARD;	PRT;	212 AA.
AC	007474:			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Floral homeotic protein PMADS 2.			
GN	PMADS2.			
OS	Petunia hybrida (Petunia).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiales; Solanales; Solanaceae; Petunia.			
OX	NCBI_TaxID=4102;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Tissue=Petal;			
RX	MEDLINE=94105323; PubMed=8278527;			
RA	Kuen A., Brunelle A., Shevell D., Chua N.-H.;			
RT	"The cDNA sequence of two MADs box proteins in Petunia."			
RL	Plant Physiol. 102:1051-1052(1993).			
CC	-1- FUNCTION: Transcription factor involved in the genetic control of flower development.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- Tissue specificity: Predominantly expressed in petals and stamens, less in carpels and sepals.			
CC	-1- SIMILARITY: Contains 1 K-box dimerization domain.			
CC	-1- SIMILARITY: Contains 1 MADs-box domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	EMBL: X69947; CAA49568.1; -			
DR	PIR: S31707; S31707.			
DR	HSSP: P11746; 1MM.			
DR	TRANSFAC: T03134; -			
DR	InterPro: IPR002487; TF_Kbox.			
DR	InterPro: IPR002100; TF_MADSbox.			
DR	Pfam: PF01486; K-box; 1.			
DR	Pfam: PF00319; SRF-TF; 1.			
DR	PRINTS: PR00404; MADSDOMAIN.			
DR	SMART: SM00432; MADS; 1.			
DR	PROSITE: PS00350; MADS_BOX_1; 1.			
DR	PROSITE: PS50066; MADS_BOX_2; 1.			
KW	Transcription regulation; DNA-binding; Activator; Nuclear protein; Developmental protein.			
FT	DOMAIN 3 58 MADS-box.			
FT	DOMAIN 93 165 K-BOX.			
SQ	SEQUENCE 212 AA; 24785 MW; FCH10C16D52E4210 CRC64;			

Query Match

67.1%; Score 740.5; DB 1; Length 212;

Best Local Similarity 67.4%; Pred. No. 4e-40;
Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1.

QY 1 MGRGKVEIKRIENSSNRQVTSKRNRNGIKKAKEITVJCDAKYSLIIYSSSGKAVEYCS 60

Db 1 MGRGKIEIKRIENSSNRQVTSKRNRNGIKKAKEITVJCDAKYSLIIFGSGKHEYCS 60

Query Match	64.6%;	Score 713;	DB 1;	Length 215;
Best Local Similarity	63.1%;	Pred. No. 2.2e-38;		
Matches 135; Conservative	40;	Mismatches 39;	Indels 0;	Gaps 0;

61 STTLEILDKXHGSGKLLMAKHNLSNEVPRVKDNDSDMOVELRHLKGDITSLNHVE 12

1 MGRGVEIKRIENSNRQVTSKRNGI1KKAETVLCDAKVSLIYSSGKMVEYCS 60

DB 6 STTPEMDLDGYQRTSGRRLDPAKHENTSNEIDRIKKENDNMQVYLRHLGKEDINSLNHKE 12

DY 121 LMALEALENGLTSIRDKOSKFEVDMKMDNGKALEDENKRLTYELIQOQEMKIKENVRNME 18

1 MGRGRIEIKLEIENSNRQVTVYSKRRNGIMKKAEISVLCDAHVSIIFASSGKMHFECSF 60
61 STLTLEILDKRYHGQSGKKLWPAKHEINISNEVDKDKDMSQVEIRHLKGEDITSJNHVE 120

Db 121 LNVLEGLTNGLSSTIAKQSEILRMVAKNDQILSEEHQLOVYALHQENAAAGGNRMIE 18

61 STTLVDMLDHYKLSGRKLMDEKHEHLDNEINRYKENDSMQIEPLRLKSGEDITILNYKE 120

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27 161 NGITRQUGINNNVOQLFEAKRVQPLQENLBERI 215
    ||||| : : ||||| ||||| ||| :
Db 161 EVYHQ---DRDYEQQMPFALRVQRPQNLHERM 212

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121 LMAEAEALENELISIRDOQKAVDMMDNGKALEDEENGLIYELQOQEMLIKENVRNME 180
    |||:|||| ::::|:||| : :||| : :||| : :||| : :||| : :||| :
121 LMVJEDALENGTSALKNQOMEIVRMKRKNEMWEEBNSQLFKLRQMHLDPMDNDNVESQ 180

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RESULT 2	
GLOB_ANTMA	
ID _GLOB ANTMA	STANDARD;
	PRT; 215 AA.

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181 NGIHQRQLGNINNNQQDLPFAFRVQIPQNLQER 214
      |      :  : | : : : : : : : : : :
181 AVYDHHHQNADYEQAQPFARFRVQIPQNLQER 214

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DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)

RESULT 3
JOB_TOBAC STANDARD: PRT: 209 AA.

0C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
GN Antirrhinum majus (Garden snapdragon).
EUKA_HOMOCYTE_PROTEIN_GLOBDB

0032167
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)

BN [1] NCBI_TaxID=4151; Antirrhinaeae; Antirrhineae; Antirrhinum.

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RX MEDLINE=93099842; PubMed=1361166;
 RA Troebner W., Ramirez L., Motte P., Hue I., Huijser P., Loennig W.-E.,
 RA Saedler H., Sommer H., Schwartz-Sommer Z.;

NCBI_TaxID=4097;
[1]

RT control of Antirrhinum floral organogenesis. ";
RL EMBO J. 11:4693-4704(1992).
CC - FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF

DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX 1; 1.
 DR PROSITE; PS00350; MADS_BOX 2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Developmental protein.
 FT DOMAIN 3 57 MADS-box.
 FT 91 163 K-BOX.
 SQ SEQUENCE 209 AA; 24691 MW; 5661FC1640E1A47 CRC64;

Query Match 64.1%; Score 707; DB 1; Length 209;
 Best Local Similarity 63.6%; Pred. No. 38; Indels 6; Gaps 2;
 Matches 136; Conservative 41; Mismatches 31;

QY 1 MGRKVEIKRIENSNROVYTSKRNGIILKKAKEITVLCDAKVSLLIYSSSGKWEYCSP 60
 DB 1 MGRKVEIKRIENSNROVYTSKRNGIILKKAKEISVLCDAKVSLLIYSSSGKWEYF--S 58
 QY 61 STLTLEILDKYHGSGKKLMDAKHENTLSEVDYRKNDNSQVLELRLKGEDITSLNHVE 120
 DB 59 STSLVDILDOYHKLTRRLMDAKHENTLSEVDYRKNDNSQVLELRLKGEDITSLNHRE 118
 QY 121 LMALEBALNGLTISIRKQSKFYDWMRDNGKALDENKRLTYELQKQCEMKIKENYVME 180
 DB 119 LMLLEDALNGLTISIRKQNDLRLMKRKTKQSMEEDQDQNLQRLQLEIASNRRNGEIG 178
 QY 181 NGYHORQLGNVNNQOQIPPAFRVQPIQPNLOER 214
 DB 179 EVFHQRE---NEYQTOMPEFAFRVQPMQPNLOER 208

RESULT 4

FBP1_PETHY STANDARD; PRT; 210 AA.

AC Q03488;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein FBP1 (Floral binding protein 1).
 OS FBP1.
 GN Petunia hybrida (petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93005737; PubMed=1356537;
 RA Angenent G.C., Buschcher M., Franken J., Mol J.N.M., van Tunen A.J.;
 RT "Differential expression of two MADS box genes in wild-type and mutant petunia flowers";
 RL Plant Cell 4:983-993(1992).
 CC -!- FUNCTION: Probable transcription factor.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: PETAL.
 CC -!- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -!- SIMILARITY: Contains 1 MADS-box domain.
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 CC
 CC EMBL; M91190; AAA3731.1; -.
 DR EIR; JQ1689; JQ1689.
 DR HSSP; P11746; INNM.
 DR TRANSFAC; T03092; -.
 DR InterPro; IPR002487; TF_KDOX.
 DR InterPro; IPR002100; TF_MADSBOX.
 DR Pfam; PF01466; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.

DR PRINTS; PR00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX 1; 1.
 DR PROSITE; PS00350; MADS_BOX 2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 KM Developmental protein.
 FT DOMAIN 3 57 MADS-box.
 FT 91 163 K-BOX.
 SQ SEQUENCE 210 AA; 24647 MW; B2D371866A157C8E CRC64;

Query Match 62.1%; Score 684.5; DB 1; Length 210;
 Best Local Similarity 62.3%; Pred. No. 1,36-36;
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;

QY 1 MGRKVEIKRIENSNROVYTSKRNGIILKKAKEITVLCDAKVSLLIYSSSGKWEYCSP 60
 DB 1 MGRKVEIKRIENSNROVYTSKRNGIILKKAKEISVLCDAKVSLLIYSSSGKWEYF--S 58
 QY 61 STLTLEILDKYHGSGKKLMDAKHENTLSEVDYRKNDNSQVLELRLKGEDITSLNHVE 120
 DB 59 STSLVDILDOYHKLTRRLMDAKHENTLSEVDYRKNDNSQVLELRLKGEDITSLNHRE 118
 QY 121 LMALEBALNGLTISIRKQSKFYDWMRDNGKALDENKRLTYELQKQCEMKIKENYVME 180
 DB 119 LMLLEDALNGLTISIRKQNDLRLMKRKTKQSMEEDQDQNLQRLQLEIASNRRNGEIG 178
 QY 181 NGYHORQLGNVNNQOQIPPAFRVQPIQPNLOER 215
 DB 179 EVFHQRE---NEYQTOMPEFAFRVQPMQPNLOER 210

RESULT 5

P1ST_ARATH STANDARD; PRT; 208 AA.

AC P48007; Q9SQ07; Q9SQ08; Q9SQ09; Q9SQ10; Q9SQ11; Q9SQ12; Q9SQ13;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PISTILLATA (Transcription factor PI).
 GN PI OR ARS20240 OR P5024.130.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Landsberg erecta;
 RX MEDLINE=95047314; PubMed=7958839;
 RA Goto K., Meyerowitz E.M.;
 RT "Function and regulation of the Arabidopsis floral homeotic gene PISTILLATA";
 RL Genes Dev. 8:1548-1560(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Landsberg erecta;
 RX MEDLINE=20233824; PubMed=10769227;
 RA Honma T., Goto K.;
 RT "The Arabidopsis floral homeotic gene PISTILLATA is regulated by discrete cis-elements responsive to induction and maintenance signals";
 RL Development 127:2021-2030(2000).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RX STRAIN=cv. Bla-1, cv. Bretagne, cv. Bs-1, cv. Bu-0, cv. Bu-2, cv. Chl-1, cv. Co-1, cv. Columbia, cv. Coracalla-1, cv. Cvi-0, cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta, cv. Li-3, cv. Ll-8, and cv. Lisee;
 RX MEDLINE=99126449; PubMed=9927474;
 RA Murgan M.D., Sudduth J.I.;
 RT "Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana";
 RL Genetics 151:839-846(1999).

RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Columbia;
 RX MEDLINE=21016721; PubMed=1130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kozani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasanoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
 RA Nakazaki N., Nambu K., Okumura S., Shino S., Takeuchi C., Mada T.,
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spieser L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Haberman K., Murray J., Johnson D., Rottling T., Nelson J.,
 RA Steneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
 RA Du H., Edwards J., Fryman J., Hakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozeraky P., Riley A., Strommatt C.,
 RA Wagner-Watson C., Wollan A., Yokum M., Bell M., Dedina N.,
 RA Farnell L., Shah R., Rodriguez M., Hoon See L., Vill D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckaert G., Wambut R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Ertlan K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.A., McCullagh B., Robben J., Grynoprez B., Zimmermann W.,
 RA Ransperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirke G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Weitzenecker M., Lamberth S., Villarroel R., Giesen J., Ardiles W.,
 RA Feldausch M., Lamberth S., Villarroel R., Giesen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F., Rüd S., Schoof H.,
 RA Schneller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 chaliana."
 RT Nature 408:823-826(2000).
 RL [5]
 RN FUNCTION.
 RP MEDLINE=96152196; PubMed=86565821;
 RX Krizek B.A., Meyerowitz E.M.,
 RA "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient
 to provide the B class organ identity function."
 RT Development 122:11-22(1996).
 RL [6]
 RN CHARACTERIZATION.
 RP MEDLINE=96209811; PubMed=8643482;
 RX Riechmann J.L., Krizek B.A., Meyerowitz E.M.,
 RA "Dimerization specificity of Arabidopsis MADS domain homeotic proteins
 APETALA3, APETALA3, PISTILLATA, and AGAMOUS."
 RT Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
 RL [7]
 RN GENETIC REGULATION.
 RP MEDLINE=21178805; PubMed=11283333;
 RX Ng M., Yancovsky M.F.,
 RA "Activation of the Arabidopsis B class homeotic genes by APETALA3."
 RT Plant Cell 13:739-753(2001).
 RL [8]
 RN CHARACTERIZATION.
 RP MEDLINE=21074934; PubMed=11206550;
 RX Honma T., Goto K.,
 RA "Complexes of MADS-box proteins are sufficient to convert leaves into
 floral organs."
 RT Nature 409:525-529(2001).
 RL -1- FUNCTION: Probable transcription factor involved in the genetic
 control of flower development. Is required for normal development
 of petals and stamens in the wild-type flower. Forms an
 heterodimer with APETALA3 that is required for autoregulation of
 both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1
 or SEPALLATA3 to form a ternary complex that could be responsible
 for the regulation of the genes involved in the flower
 development.
 CC -1- SUBUNIT: Forms an heterodimer with APETALA3, capable of binding to
 CAG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to form a
 ternary complex.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- INDUCTION: Positively regulated by the meristem identity
 proteins APETALA1 and LEAFY with the cooperation of UFO.
 CC -1- MISCELLANEOUS: Mutations in PI cause transformation of petals into

CC sepals and stamens into carpels.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----
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 or send an email to license@isb.ch).
 CC -----
 DR EMBL; D30807; BA06465.1; -
 DR EMBL; AB035137; BA087000.1; -
 DR EMBL; AF115815; AAD51984.1; -
 DR EMBL; AF115816; AAD51985.1; -
 DR EMBL; AF115817; AAD51986.1; -
 DR EMBL; AF115818; AAD51987.1; -
 DR EMBL; AF115819; AAD51988.1; -
 DR EMBL; AF115820; AAD51989.1; -
 DR EMBL; AF115821; AAD51990.1; -
 DR EMBL; AF115822; AAD51991.1; -
 DR EMBL; AF115823; AAD51992.1; -
 DR EMBL; AF115824; AAD51993.1; -
 DR EMBL; AF115825; AAD51994.1; -
 DR EMBL; AF115826; AAD51995.1; -
 DR EMBL; AF115827; AAD51996.1; -
 DR EMBL; AF115828; AAD51997.1; -
 DR EMBL; AF115829; AAD51998.1; -
 DR EMBL; AF115830; AAD51999.1; -
 DR EMBL; AF296825; -; NOT_ANNOTATED_CDS.
 DR PIR; A53839; A53839.
 DR HSSP; P11746; 1MMN.
 DR TRANSFAC; T03129; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 KW Flowering; Transcription regulation; Activator; Developmental protein;
 KW Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
 FT DOMAIN 3 57
 FT DOMAIN 106 143
 FT DOMAIN 75 117
 FT DOMAIN 29 29
 FT VARIANT 38 38
 FT VARIANT 51 51
 FT VARIANT 73 73
 FT VARIANT 75 75
 FT VARIANT 89 89
 FT VARIANT 112 112
 FT VARIANT 125 125
 FT VARIANT 140 140
 FT VARIANT 142 142
 FT VARIANT 160 160
 FT VARIANT 203 203
 SQ SEQUENCE 208 AA; 24047 MW; 49728735AC883CCA CRC64;
 Query Match 59.9%; Score 660.5; DB 1; Length 208;
 Best Local Similarity 60.5%; Pred. No. 4,1e-35;
 Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;
 QY 1 MGRGKVEIKRIENSNROVTSKRNGIKKAKETIVCDKAVSIIYSSGKWEYCSP 60
 DB 1 MGRGKVEIKRIENSNRNVVTSKRNGVKKAKETIVCDKAVAIIRASNGKMDYCCP 60
 QY 61 STTLEILDKYGGSGGCKLMDAKHENSNEVDYKXNDNQVLEIRHKGEDITSLAHE 120
 DB 61 SMIDGAMLDQYOKLSGKTLMDAKHENSNEIDRIKENDSLOLEIRHKGEDISLKN 120

QY 121 LMALEALENGSLTSDKOSKFDVMDNGKALEDENKRLTYELQCEMKIKENRYNME 180
 DB 121 LMAVEAHIEHGLKVDHDKHWEIISKRKREKMAESROUUTFOLQ-QCEMALASNARGMM 179
 QY 181 NGYHOSQOLGNNNNQOIPPAFVQPIOPNLOERI 215
 DB 180 MRDHDCQ-----FGYRVQPIQPVLCCKI 202

RESULT 6
 M13_GNEGN STANDARD; PRT; 237 AA.
 ID M13_GNEGN
 AC Q9XGJ4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein GGM13.
 GN GGM13.
 OS Gnetum gnemon (Bago).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Gnepophyta; Gnepopsida; Gnetales; Gnetales; Gnetum.
 OX NCBI_TaxID=3382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99307411; PubMed=10377416;
 RA Winter K.-U., Becker A., Muenster T., Kim J.T., Saedler H.,
 Theissen G.;
 RT "MADS-box genes reveal that gnetophytes are more closely related to
 RT confers than to flowering plants.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:7342-7347(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=21851234; PubMed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 Saedler H., Theissen G.;
 RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes.";
 RL Mol. Genet. Genomics 266:942-950(2002).
 CC [1] FUNCTION: Probable transcription factor.
 CC [1] SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC [1] TISSUE SPECIFICITY: Expression specific for female reproductive
 CC structures: strong at the adaxial base of the cupules, where
 CC ovules will later develop, then in the outermost cell layer of the
 CC nucellus, in the inner envelope, and in the inner half of the
 CC middle envelope at late stage of ovule development.
 CC [1] SIMILARITY: Contains 1 K-box dimerization domain.
 CC [1] SIMILARITY: Contains 1 MADS-box domain.
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 CC
 CC EMBL: AJ132219; CAB4459.1; -.
 CC HSSP: F11746; IWMN.
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 CC Pfam: PF01486; K-box; 1.
 CC Pfam: PF00319; SRF-TF; 1.
 CC PRINTS: PR00404; MADSbox.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC DOMAIN 1 61 MADS-box.
 CC FT DOMAIN 1 170 K-BOX.
 CC SQ SEQUENCE 237 AA; 26943 MW; 5C65191A5ID08691 CRC64;

Query Match 38.2%; Score 421; DB 1; Length 237;
 Best Local Similarity 37.7%; Pred. No. 5; 2e-20;

Matches 90; Conservative 52; Mismatches 57; Indels 40; Gaps 4;
 QY 1 MGRGVEIKRIENSSNROVYTSKRRNGITIKAKIITVLCDAKVALIYSSSGKVRVYCSF 60
 DB 1 MGRGVEIKRIENSSNROVYTSKRRNGITIKAKIITVLCDAKVALIYSSSGKVRVYCSF 60
 QY 61 STTLEIILDKHGOSGKGLMDAKENLSNEVDVYKNDSDQVQLRHUKSDITSLNHYE 120
 DB 61 SSMKITERQYKSGARITEYDQHLVCEYTRKAKENKIQTNIRRMGGDLTSLNHYE 120
 QY 121 LMALEALENGSLTSDKOSKFDVMDNGKALEDENKRLTYELQCEMKIKENRYNME 168
 DB 121 LHLHGOQLSASASVRSRKNQIMQOLENLRKERILEDQSHLCRLAEQQAIVEGVOE 180
 QY 169 -----EMKIKENRYNMEGYHQRQGLGNNNNQOIPPAFVQPIOPNLOE 213
 DB 181 PLLEGVCFPPDNNKTAANAAGPLHGH-----LP-AFRLQPTQPNLOE 225

RESULT 7
 M17_MAIZE STANDARD; PRT; 259 AA.
 ID M17_MAIZE
 AC Q8VWM8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein ZMM17.
 GN M17.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_7232; TISSUE=Flower;
 RX MEDLINE=21851234; PubMed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 Saedler H., Theissen G.;
 RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes.";
 RL Mol. Genet. Genomics 266:942-950(2002).
 CC [1] FUNCTION: Probable transcription factor.
 CC [1] SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC [1] TISSUE SPECIFICITY: Strong expression in female inflorescences
 CC (ears), but also weak expression in male inflorescences (tassels).
 CC At early stages of the development of the female spikelet,
 CC and the developing silk. At very late stages of development,
 CC expression becomes restricted to parts of the silk.
 CC [1] SIMILARITY: Contains 1 K-box dimerization domain.
 CC [1] SIMILARITY: Contains 1 MADS-box domain.
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 CC
 CC EMBL: AJ271208; CAC91053.1; -.
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 CC Pfam: PF01486; K-box; 1.
 CC Pfam: PF00319; SRF-TF; 1.
 CC PRINTS: PR00404; MADSbox.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC DOMAIN 1 61 MADS-box.
 CC FT DOMAIN 1 171 K-BOX.

SEQUENCE 259 AA; 29001 MW; B94E74F1D9420D44 CRC64;

Query Match 34.9%; Score 384.5; DB 1; Length 259;
Best Local Similarity 33.6%; Pred. No. 11e-17;
Matches 82; Conservative 56; Mismatches 75; Indels 31; Gaps 4;

QY 1 MGRGVEIKRIENSNROVYTSKRNGIIRKAKETIVLCDAKVSIIYSSGKWEYCSF 60

DB 1 MGRGVEIKRIENSNROVYTSKRNGIIRKAKETIVLCDAKVSIIYSSGKWEYCSF 60

QY 61 STTLTFLDKYHGSGSKLMDAKH-ENLSNEVDYKNDSDMQVELRHLKGEDITSLNHV 119

DB 61 STTLTFLDKYHGSGSKLMDAKH-ENLSNEVDYKNDSDMQVELRHLKGEDITSLNHV 119

QY 120 EIMALEEALENGSLTIRDSKSFVDMRDN-----GKALEDEKRLTYELQKQEKIKEN 175

DB 120 EIMALEEALENGSLTIRDSKSFVDMRDN-----GKALEDEKRLTYELQKQEKIKEN 175

QY 121 DVSDEIQQLIEYVSRYKARKKQLNQLDNRKQQLIEDQTPLYKMINENQQAALTE 180

DB 121 DVSDEIQQLIEYVSRYKARKKQLNQLDNRKQQLIEDQTPLYKMINENQQAALTE 180

QY 176 VR-----NNENGYHORQLGNNYNNQOQIPPA-----PVOPIOP 209

DB 181 VILGEMAPLAMPPEPAFAHSATAYGSSSSGTALQLMSAAPQLHADLDLGFPLQPTOP 240

QY 210 NICE 213

DB 241 NLQD 244

RESULT 8

MAD1_PETHY ID MAD1_PETHY STANDARD; PRT; 231 AA.

AC 007472;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Floral homeotic protein PMADS 1 (Green petal homeotic protein).

GN PMADS1 OR GP.

OS Petunia hybrida (Petunia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Solanales; Solanaceae; Petunia.

OX NCBI_TaxID=4102;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Petal;

RX MEDLINE=94105323; PubMed=8278527; Chua N.-H.;

RA Kuhn A., Bruneille A., Sneveil D., Chua N.-H.;

RT "The CDNA sequence of two MADS box proteins in Petunia.";

RL Plant Physiol. 102:1051-1052(1993).

CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF

CC FLOWER DEVELOPMENT. NECESSARY FOR THE NORMAL DEVELOPMENT OF

CC PERIPLASMA OF THE PMADS1 PROTEIN CAUSES TRANSFORMATION OF

CC PERIPLASMA INTO SEPAL.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: Predominantly expressed in petals and stamens,

CC less in carpels and sepals.

CC -1- SIMILARITY: Contains 1 K-box dimerization domain.

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CC -----

DR EMBL: X69946; CAA49567.1; -

DR PIR: S31693; S31693.

DR HSSP: P11746; 1MMN.

DR TRASPAC: T01777; -

DR InterPro: IPR002487; TF_Kbox.

DR InterPro: IPR002100; TF_MADSbox.

DR Pfam: PF01486; K-box; 1.

DR Pfam: PF00319; SRP-TF; 1.

DR PRINTS: PR00404; MADS-DOMAIN.

DR SMART: SM00432; MADS_1.

DR PROSITE: PS00350; MADS_BOX_1; 1.

DR PROSITE: PS00350; MADS_BOX_2; 1.

DR Transcription regulation; DNA-binding; Activator; Nuclear protein;

DR Developmental protein.

FT DOMAIN 3 58 MADS-box.

FT DOMAIN 93 165 K-box.

FT SEQUENCE 231 AA; 27039 MW; 76AE5EB043488B6F CRC64;

Query Match 34.2%; Score 377.5; DB 1; Length 231;

Best Local Similarity 38.5%; Pred. No. 2.7e-17;

Matches 84; Conservative 47; Mismatches 72; Indels 15; Gaps 4;

QY 1 MGRGVEIKRIENSNROVYTSKRNGIIRKAKETIVLCDAKVSIIYSSGKWEYCSF 60

DB 1 MGRGVEIKRIENSNROVYTSKRNGIIRKAKETIVLCDAKVSIIYSSGKWEYCSF 60

QY 61 STTLTFLDKYHGSGSKLMDAKH-ENLSNEVDYKNDSDMQVELRHLKGEDITSLNHV 120

DB 61 STTLTFLDKYHGSGSKLMDAKH-ENLSNEVDYKNDSDMQVELRHLKGEDITSLNHV 120

QY 121 LMALEEALENGSLTIRDSKSFVDMRDN-----GKQIEIFPKKVNVEIHRVLEPDAQED 180

DB 121 LMALEEALENGSLTIRDSKSFVDMRDN-----GKQIEIFPKKVNVEIHRVLEPDAQED 180

QY 121 LEMEMENVNSLKLIRKRYKV-----GNQIEIFPKKVNVEIHRVLEPDAQED 174

DB 121 LEMEMENVNSLKLIRKRYKV-----GNQIEIFPKKVNVEIHRVLEPDAQED 174

QY 181 NGYHORQLGNNYNNQOQIPPAFVCP--IQPN 210

DB 175 PGLVGEQEDGYNVSLGFGPFGHRI-LALRLQENHQP 211

RESULT 9

DE21_ANTWA ID DE21_ANTWA STANDARD; PRT; 247 AA.

AC 08RVL4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE MADS box protein defn21 (DEFICIENS homolog 21).

GN DEF21.

OS Antirrhinum majus (Garden snapdragon).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Antirrhineae; Antirrhineae; Antirrhinum.

OX NCBI_TaxID=4151;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Flower buds;

RX MEDLINE=21851234; PubMed=11862488;

RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.A.,

RT "A novel MADS-box gene subfamily with sistergroup relationship to

RT class B floral homeotic genes.";

RL Mol. Genet. Genomics 266:942-950(2002).

CC -1- FUNCTION: Probable transcription factor.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed exclusively in a few inner cell

CC layers of the inner integuments of the ovules.

CC -1- SIMILARITY: Contains 1 K-box dimerization domain.

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CC -----

DR EMBL: AJ307056; CA85225.1; -

DR InterPro: IPR002487; TF_Kbox.

DR InterPro: IPR002100; TF_MADSbox.

DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01466; K-box; 1.
DR Pfam: PF00319; SRF-TE; 1.
DR PRINTS: PR00432; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 4 MADS-box.
FT DOMAIN 72 K-BOX.
FT DOMAIN 187 196 HIS-RICH.
SQ SEQUENCE 268 AA; 31119 MW; 4C85ADB87F63F16A CRC64;

Query March 32.7%; Score 360.5; DB 1; Length 268;
Best Local Similarity 33.2%; Pred. No. 3,7e-16;
Matches 85; Conservative 53; Mismatches 75; Indels 43; Gaps 6;

QY 1 MGRGVEIKRIENSSNQVYTKRRNGIKKAKIYLCDAKSLIYSSGKXVRYCSP 60
DB 4 MGRKIKVKEIKENTKSQVTFKSRAGLLKTKHETSLVCAQIGLITFSSGKLFYCQ 63

QY 61 STLTELIDKXHQSGKKLWDAGHEHLSNVDYRKNDNSMQVELHAKCEDTSLNHV 119
DB 64 PHSQSILTSRLQTTGSLPEVDNRVOLYBVAKKARDTTLQSLDRYKDDLSLAQYE 123

QY 120 ELMALEALENGLTSIRDKOSKFEVMDKRDNGKALEDENKRLTYELQKQEMKIKEN 175
DB 124 ELNLEKQLEHAIANKIARKLLEMQQKEMLKTEKMLEKENHMYQWLMNNQMYKQESA 183

QY 176 VRNNGYHQHQ-----LG-----NYYNNQQQIP-----FA----- 201
DB 184 AMDEHDHHRHHEHQATTELNLLGEPLLSHTFFFGQEQPSTVNHFFASISLTPSPAN 243

QY 202 ----FRVQPIOPNCE 213
DB 244 SISPYRLQPSHNLD 259

RESULT 11
AP3_ARATH STANDARD; PRT; 232 AA.
ID AP3_ARATH STANDARD; PRT; 232 AA.
AC P1633; Q98003; OSLB79; Q98703; Q98014; Q98015; Q98016; Q98017;
AC Q98018; Q98019; Q98020; Q98021; Q98022; Q98X13;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Floral homeotic protein APTAL3.
GN AP3 OR AT3G54340 OR T1ZE18.30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal.
RC MEDLINE=92154682; PubMed=1346756;
RX Jack T., Brockman L.L., Meyerowitz E.M.;
RA "The homeotic gene APTAL3 of Arabidopsis thaliana encodes a MADS
RT box and is expressed in petals and stamens.";
RL Cell 68:683-697(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX Okamoto H., Yano A., Shiraiishi H., Okada K., Shimura Y.;
RA "Genetic complementation of a floral homeotic mutation, apetal3,
RT with an Arabidopsis thaliana gene homologous to DEFICIENS of
RL Antirrhinum majus";
RL Plant Mol. Biol. 26:465-472(1994).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,
RC

RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
RC cv. Li-3, cv. Li-8, and cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci: departures
RT from the equilibrium-neutral model at the *APETALA3* and *PISTILLATA*
RT genes of *Arabidopsis thaliana*.";
RL Genetics 151:839-848(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Farmanhat M., Lemcke K., Rieger H., Ansoerg W., Unseid M.,
RA Farmanhat M., Valle G., Bloeker H., Peter-Alonso M., Oberwälder B.,
RA Delenly M., Boutry M., Griwell L.A., Maché R., Purganensch P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Broetier P.,
RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wurmacher E., Drzonek H., Erle H., Jordan N., Banger S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharte M., Schoen G., Barques M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwälder B., Masny D.,
RA Cooke R., Laude M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maeres A.C., Alcaraz J.-P., Cortet A., Gacubeta E.,
RA Montfort A., Agirion A., Flores R., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
RA Cressey T.H., Haas B., Malt R., Malt R., Malt R., Malt R.,
RA Pal G., Miltischer J., Sellers P., Gall J.E., Feldlym T.V.,
RA Prens D., Lin X., Nieman W.C., Salberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Nishio S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis thaliana*.";
RL Nature 408:820-823(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldman K.A.;
RT "Full-length cDNA from *Arabidopsis thaliana*.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Nemman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari P.,
RA Arakawa T., Bah J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enyu A., Goldsmith A.D., Guiral M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuang V.M., Iida K., Karnes M.,
RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the *Arabidopsis*
RT genome.";
RL Science 302:842-846(2003).
RN [7]
RP SEQUENCE OF 36-128 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99311297; PubMed=10362288;
RA Brunel D., Proger N., Pelletier G.;
RT "Development of amplified consensus genetic markers (ACGM) in *Brassica*

RT napus from *Arabidopsis thaliana* sequences of known biological
RT function.";
RL Genome 42:387-402(1999).
RN [8]
RP FUNCTION.
RX MEDLINE=96152196; PubMed=8565821;
RA Krizek B.A., Meyerowitz E.M.;
RT "The *Arabidopsis* homeotic genes *APETALA3* and *PISTILLATA* are sufficient
RT to provide the B class organ identity function.";
RL Development 122:11-22(1996).
RN [9]
RP CHARACTERIZATION.
RX MEDLINE=96209811; PubMed=8643482;
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
RT "Dimerization specificity of *Arabidopsis* MADS domain homeotic proteins
RT *APETALA1*, *APETALA3*, *PISTILLATA*, and *AGAMOUS*.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
RN [10]
RP GENETIC REGULATION.
RX MEDLINE=21178805; PubMed=11283333;
RA Ng M., Yanofsky M.F.;
RT "Activation of the *Arabidopsis* B class homeotic genes by *APETALA1*,"
RL Plant Cell 13:739-753(2001).
RN [11]
RP CHARACTERIZATION.
RX MEDLINE=21074934; PubMed=11206550;
RA Honma T., Goto K.;
RT "Complexes of MADS-box proteins are sufficient to convert leaves into
RT floral organs.";
RL Nature 409:525-529(2001).
RN [12]
RP FUNCTION: Probable transcription factor involved in the genetic
CC control of flower development. Is required for normal development
CC of petals and stamens in the wild-type flower. Forms an
CC heterodimer with *PISTILLATA* that is required for autoregulation of
CC both *AP3* and *PI* genes. *AP3/PI* heterodimer interacts with *APETALA1*
CC or *SEPALLATA3* to form a ternary complex that could be responsible
CC for the regulation of the genes involved in the flower
CC development.
CC -1- SUBUNIT: Forms an heterodimer with *PISTILLATA*, capable of binding
CC to CARG-box sequences. *AP3/PI* heterodimer binds *AP1* or *SEP3* to
CC form complexes.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed in petals and stamens.
CC -1- INDUCTION: Positively regulated by the meristem identity proteins
CC *APETALA1* and *LEAFY* with the cooperation of UFO.
CC -1- MISCELLANEOUS: Mutations in *AP3* cause transformation of petals
CC into sepals and stamens into carpels.
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
CC -1- SIMILARITY: Contains 1 MADS-box domain.
CC -----
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CC -----
DR EMBL: M66357; AAA32740.1; -
DR EMBL: D21125; BAB04665.1; -
DR EMBL: AF115798; AAD51887.1; -
DR EMBL: AF115799; AAD51888.1; -
DR EMBL: AF115800; AAD51889.1; -
DR EMBL: AF115801; AAD51890.1; -
DR EMBL: AF115802; AAD51891.1; -
DR EMBL: AF115803; AAD51892.1; -
DR EMBL: AF115804; AAD51893.1; -
DR EMBL: AF115805; AAD51894.1; -
DR EMBL: AF115806; AAD51895.1; -
DR EMBL: AF115807; AAD51896.1; -
DR EMBL: AF115808; AAD51897.1; -
DR EMBL: AF115809; AAD51898.1; -
DR EMBL: AF115810; AAD51899.1; -

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DR EMBL; AF115811; AAD51900.1; -
DR EMBL; AF115812; AAD51901.1; -
DR EMBL; AF115813; AAD51902.1; -
DR EMBL; AF115814; AAD51903.1; -
DR EMBL; AL132971; CAB81799.1; -
DR EMBL; AY087369; AAL64919.1; -
DR EMBL; AY070397; AAL49893.1; -
DR EMBL; AY142590; AAN13159.1; -
DR EMBL; AF056541; AAD41557.1; -
DR PIR; A42095; A42095.
DR HSSP; P11746; 1NMW.
DR TRANSFAC; T01008; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Flowering; Transcription regulation; Activator; Developmental protein;

Query Match 32.3%; Score 356.5; DB 1; Length 232;
Best Local Similarity 35.1%; Pred. No. 5,7e-16;
Matches 79; Conservative 46; Mismatches 73; Indels 27; Gaps 3;

QY 1 MGRKVEIKRIENSSNRQVTYSRRNGIIRKAEITVLCDAKVSLLIYSSSGKVEYCSF 60
DB 1 MARGKIQIKRIENQTRQVYTSKRNGIFPKAHEITVLCDAKVSIIIMPSSNKLHEYISF 60

QY 61 STLTLELDKYHGGSGKKLMDAKHEMLSNVDYVKKDNDSMQVELRLHKGEDITSLNHVE 120
DB 61 NTTKTKELVDYQITSDVDWATQIERKQETKTKLTLNRLKQIQIRLGSCLDELDIGE 120

QY 121 LMALEBALENGLTISIRPKOSKSF---VDMARDNGKALEDENKLTLYELOKQOEMKIKENV 176
DB 121 LRLEDEMENTFTLVBERKFKSLGNQIEETTKKNGKQODIQKLHLELRBAE---DPHY 177

QY 177 RMNENG-----YHQQLGNYNNNQOQIFPA 201
DB 178 GLVDNGQDYDSVLGYQIEGSRAYALRFHONHHYHNGHLMAPSA 222

RESULT 12
DEFA_ANTMA STANDARD; PRT; 227 AA.
AC P23706;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Floral homeotic protein deficiencies.
GN DEFA.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Antirrhinales; Antirrhinae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90183955; PubMed=1968830;
RA Sommer H., Beltran J.-P., Hulsner P., Pape H., Loeonig W.-E.,
RA Saedler H., Schwarz-Sommer Z.;
RT "Deficiens, a homeotic gene involved in the control of flower
RT morphogenesis in Antirrhinum majus: the protein shows homology to
RT transcription factors.";
RL EMBL J. 9:605-613(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sippe 50;
RX MEDLINE=92155166; PubMed=1346760;
RA Schwarz-Sommer Z., Hue I., Hulsner P., Flor P.J., Hansen R.,
RA Teters F., Loeonig W.-E., Saedler H., Sommer H.;
RT "Characterization of the Antirrhinum floral homeotic MADS-box gene

```

```

RT deficiens: evidence for DNA binding and autoregulation of its
RT persistent expression throughout flower development.";
RL EMBL J. 11:251-263(1992).
CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH GLOBOSA (GLO).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: MUTATIONS IN DEFA CAUSE TRANSFORMATION OF PETALS
CC INTO SEPALs AND STAMINA INTO CARPELS.
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
CC -1- SIMILARITY: Contains 1 MADS-box domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52023; CAA36268.1; -
DR EMBL; X62810; CAA44629.1; -
DR PIR; S12378; S12378.
DR HSSP; P11746; 1NMW.
DR TRANSFAC; T01008; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Developmental protein.
FT DOMAIN 3 57 MADS-box.
FT DOMAIN 93 165 K-BOX.
SQ SEQUENCE 227 AA; 26279 MW; 95B3PF60924FDEB CRC64;

Query Match 31.6%; Score 349; DB 1; Length 227;
Best Local Similarity 39.3%; Pred. No. 1.6e-15;
Matches 68; Conservative 42; Mismatches 59; Indels 4; Gaps 1;

QY 1 MGRKVEIKRIENSSNRQVTYSRRNGIIRKAEITVLCDAKVSLLIYSSSGKVEYCSF 60
DB 1 MARGKIQIKRIENQTRQVYTSKRNGIFPKAHEITVLCDAKVSIIIMPSSNKLHEYISF 60

QY 61 STLTLELDKYHGGSGKKLMDAKHEMLSNVDYVKKDNDSMQVELRLHKGEDITSLNHVE 120
DB 61 TTATKQLDQYQKAVGVDLMSHVEKQEHKKLVNVRNLRRIROMGESLNDLGYEQ 120

QY 121 LMALEBALENGLTISIRPKOSKSFVDMARDNGKA---LEDEKRLTYELOKQOE 169
DB 121 IVNLIEDMNSLKILIRERKRVISNQIDTSKKKVRNVEIHRNLVLEFDARE 173

RESULT 13
TT16_ARATH STANDARD; PRT; 252 AA.
AC Q8RTD9; Q8RFK4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE TRANSPARENT TESTA 16 protein (Arabidopsis BSISTER MADS box protein).
GN TT16 OR ABS OR AT5G3260 OR MCD15.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eucoside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=cv. Columbia; TISSUE=Green siliques;
RX MEDLINE=21851234; PubMed=11862488;

```

RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 RA Saedler H., Theissen G.,
 RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes.",
 RL Mol. Genet. Genomics 266:942-950 (2002).
 RN [2].
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones.",
 RL DNA Res. 4:401-414 (1997).
 RN [3].
 RP CHARACTERIZATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=2256155; PubMed=12368498;
 RA Nest N., Debeaujon I., Jond C., Stewart A.J., Jenkins G.I.,
 RA Caboche M., Lepointec L.,
 RT "The TRANSPARENT TESTA16 locus encodes the ARABIDOPSIS BISTER MADS
 RT domain protein and is required for proper development and
 RT pigmentation of the seed coat.",
 RL Plant Cell 14:2463-2479 (2002).
 CC -1- FUNCTION: Transcription factor involved in the developmental
 CC regulation of the endothelium and in the accumulation of
 CC proanthocyanidins (PAs) or condensed tannins which give the seed
 CC its brown pigmentation after oxidation. Necessary for the normal
 CC activation of the BANYANS promoter in the endothelium body.
 CC -1- PATHWAY: Flavonoid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8RYP9-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8RYP9-2; Sequence=VSP_006257;
 CC -1- TISSUE SPECIFICITY: Expressed in buds, flowers and immature seeds,
 CC but not in roots, stems, leaves, seedlings or silique valves.
 CC Expression in seed coat is confined to the endothelium layer.
 CC DEVELOPMENTAL STAGE: Expressed during seed development.
 CC -1- MISCELLANEOUS: The two isoforms were always coexpressed in the
 CC tissues investigated. The pigmentation of the chalazal-micropyle
 CC region is not under the control of ABS, as opposed to the
 CC pigmentation of the seed body.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -1- CAUTION: Ref 2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AJ318098; CAC85664.1; -
 CC EMBL: AB007648; BAB1181.1; ALT_SEQ.
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 CC Pfam: PF01486; K-box_1.
 CC Pfam: PF0319; SRP-1F; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS00065; MADS_BOX_2; 1.
 CC Flavonoid biosynthesis; Transcription; Transcription regulation;
 CC DNA-binding; Alternative splicing; Nuclear protein; Coiled coil.
 FT DOMAIN 1 61
 FT DOMAIN 73 172
 FT DOMAIN 121 174
 COILED COIL (POTENTIAL).

FT DOMAIN 180 222 GIN-RICH.
 FT VARSPIC 142 146 Missing (in isoform 2).
 FT FTID=VSP_006257.
 SQ SEQUENCE 252 AA; 29697 MW; 2C4ECB9D9C1DEB48 CRC64;
 Query Match 31.0%; Score 342; DB 1; Length 252;
 Best Local Similarity 32.0%; Pred. No. 5; Le-15;
 Matches 78; Conservative 62; Mismatches 72; Indels 32; Gaps 7;
 QY 1 MGRGKVEIKRIENSNRQVTSKRNIGIYKAKEITVLCDAVSLIYSSGKMYECSF 60
 DB 1 MGRGKVEIKRIENSNRQVTSKRNIGIYKAKEITVLCDAVSLIYSSGKMYECSF 60
 QY 61 STLTLEILPKYHQSGSKLMD--AKHENLSNEVDYKKNDSNOVELRLKGEITSLNH 118
 DB 61 QNRMPQIDRYLHTNGLRPDHDHDEQLHHEMLLRCTCLRLRPFHGHDLASIFP 120
 QY 119 VELMALEALENGSLTIRDSKSPVMDRN---GKALEDNKRLTYELQSQ-EMKIK 173
 DB 121 NEIDGLERQLEHSLVKYRKRKHELMQOLENLSRKRMLEEDNNMYRWLHFRAMEFO 180
 QY 174 ENVRNMENGVHOR---CL-----GNYN---NNQGOIPFA-----FVQPIQ 208
 DB 181 QAGIDTPGPGYQFTIQLCCYRGGTYQLPESQOQPPNSVLQATLPSPIDPTVILQAA 240
 QY 209 PNLQ 212
 DB 241 PNLQ 244
 RESULT 14
 ID SEPI ARATH STANDARD; PRT; 251 AA.
 AC 022456; O8GW04; O8L9R2;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Developmental protein SEPIALAT3 (Agamous-like MADS box protein AGL3).
 GN SEPI OR AGL3 OR ATIG24260 OR F316.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=cv. Landsberg erecta;
 RA Mandel M.A., Yanofsky M.F.;
 RT "The Arabidopsis AGL3 MADS box gene is expressed in young flower
 RT primordia".
 RL Sex. Plant Reprod. 11:22-28 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=1130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 RA Dunn P., Elguo P., Feldblum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenskaia I., Kutz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Miltschker J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vayberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";

RL Nature 408:816-820(2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,

RT Feldmann K.A.;

RT "Full-length cDNA from Arabidopsis thaliana,"

RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RL [4]

RN SEQUENCE OF 114-251 FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=22954850; PubMed=14593172;

RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

RA Chao Q., Choy N., Ebti A., Goldsmith A.D., Gurfil M., Hansen N.F.,

RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

RA Khan S., Kossema E., Ishida U., Jiang P.X., Jones T., Kawai J.,

RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Thollogis A., Ecker J.R.;

RT "Empirical analysis of transcriptional activity in the Arabidopsis

RT genome.";

RT Science 302:842-846(2003).

RL [5]

RN CHARACTERIZATION.

RX MEDLINE=98079237; PubMed=9418042;

RA Fan H.-Y., Hu Y., Tudor M., Ma H.;

RT "Specific interactions between the K domains of AG and AGUs, members

RT of the MADS domain family of DNA binding proteins.",

RT Plant J. 12:999-1010(1997).

RL [6]

RN CHARACTERIZATION.

RX MEDLINE=20279298; PubMed=10821278;

RA Pelaz S., Ditta G.S., Baumann E., Wisman E., Yanofsky M.F.;

RT "B and C floral organ identity functions require SEPALLATA MADS-box

RT genes.";

RT Nature 405:200-203(2000).

RL [7]

RN CHARACTERIZATION.

RX MEDLINE=21074934; PubMed=11206550;

RA Honma T., Goto K.;

RT "Complexes of MADS-box proteins are sufficient to convert leaves into

RT floral organs.";

RT Nature 409:525-529(2001).

RL -1- FUNCTION: Probable transcription factor active in inflorescence

CC development and floral organogenesis. Functions with

CC SEPALLATA1/AG2 and SEPALLATA2/AG4 to ensure proper development

CC of petals, stamens and carpels and to prevent the indeterminate

CC growth of the flower meristem. Interacts with APETALA3, AGAMOUS or

CC APETALA3/PISTILLATA to form complexes, that could be involved in

CC genes regulation during floral meristem development.

CC -1- SUBUNIT: Heterodimer with API or AG capable of binding to CARG-box

CC sequences. Binds AP3/PI to form a ternary complex.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=O22456-1; Sequence=displayed;

CC Name=2;

CC IsoId=O22456-2; Sequence=VSP_008893;

CC Note=May be due to a competing acceptor splice site. No

CC experimental confirmation available;

CC -1- DEVELOPMENTAL STAGE: Expressed early during flower development

CC within petals, stamens and carpels.

CC -1- MISCELLANEOUS: Triple mutations in the SEP1, SEP2 and SEP3 genes

CC result in the replacement of the stamens and petals by sepals and

CC of the carpels by a new mutant flower with sepaloid organs.

CC -1- SIMILARITY: Contains 1 K-box dimerization domain.

CC -1- SIMILARITY: Contains 1 MADS-box domain.

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CC -----

CC EMBL, AF015552; AAB67832.1; -

CC EMBL, AC002396; AAC00586.1; -

CC EMBL, AY088272; AAM65812.1; -

CC EMBL, AK118696; BAC43290.1; ALT_INIT.

CC PIR, T00656; T00656.

CC HSSP, P11746; IMMW.

CC TRANSFAC, T03032; -

CC InterPro, IPR002487; TF_KDOX.

CC InterPro, IPR002100; TF_MADSbox.

CC Pfam, PF01486; K-box; 1

CC Pfam, PF00319; SRP-TRF; 1.

CC PRINTS, PR00404; MADSDOMAIN.

CC SMART, SM00432; MADS; 1.

CC PROSITE, PS00350; MADS_BOX_1; 1.

CC PROSITE, PS0066; MADS_BOX_2; 1.

CC Flowering; Transcription regulation; Activator; Developmental protein;

CC Nuclear protein; DNA-binding; Coiled coil; Alternative splicing.

CC DOMAIN 3 57 MADS-box.

CC FT DOMAIN 100 172 K-BOX.

CC FT DOMAIN 94 177 COILED COIL (POTENTIAL).

CC FT VARSPLC 90 Missing (in isoform 2).

CC FT FT /FtId=VSP_008893.

CC SQ SEQUENCE 251 AA; 29066 MW; 0057CABD31AFC4 CRC64;

CC -----

CC Query Match 30.4%; Score 335; DB 1; Length 251;

CC Best Local Similarity 37.4%; Pred. No. 1,4e-14;

CC Matches 86; Conservative 49; Mismatches 67; Indels 28; Gaps 8;

CC QY 1 MGKGVKEIKRIENSNQVYTSKRRNGIKKAKETVLCDAKVALIIYSSGKXVVEYCSF 60

CC DB 1 MGRGVEIKRIENKINQVTFPAKRNGIKKAYLSVLCDEVALIIFSNNGKXYPFS- 59

CC QY 61 STLTETIDKTHGSGGKKLMDAKENL-----SNEVDVKKNDSDMGEVLRHL 108

CC DB 60 SSSMIRTLERYO---KKNYGAPPPNPVPSREALAVELSSQGEYIKLXERYPDALORTORNL 115

CC QY 109 KGEIDTSLNHYELMALFEALENGTLSTRDKOSKF-VDMMRD---NGALEDEKRLTYEEL 164

CC DB 116 LGEDIGPLSTKESLSERQLDSLSKQTRALATQYMLQDLNLSGKEMLTETTKTLRL 175

CC QY 165 QKQGEKIKENYNNMENGTHQROLGNTNNNOQGI-PFAFRVQPI--QPNLQ 212

CC DB 176 ADGVQMPQLNPNOBEVDHY----GRHHQOQCHSQAF-FQPLCEPILQ 220

CC RESULT 15

CC JOIN_LYCES

CC ID JOIN_LYCES STANDARD; PRT; 265 AA.

CC AC Q9FYU6;

CC DT 28-FEB-2003 (Rel. 41, Created)

CC DT 28-FEB-2003 (Rel. 41, Last sequence update)

CC DT 15-MAR-2004 (Rel. 43, Last annotation update)

CC DE MADS-box JOINTLESS protein (LEMADS).

CC GN J.

CC OS Lycopersicon esculentum (Tomato).

CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

CC CC Lamiales; Solanales; Solanaceae; Solanum.

CC OX NCBI_TaxID=4081;

CC RN [1]

CC RP SEQUENCE FROM N.A.

CC RP STRAIN=cv. Heinz 1706;

CC RX MEDLINE=20426111; PubMed=10972295;

CC RA Mao L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,

CC Irish E.E., Wing R.A.;

RT "JOINTLESS is a MADS-box gene controlling tomato flower abscission
zone development." ;
RL Nature 406:910-913 (2000).
CC -|- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT COORDINATES GENE
CC EXPRESSION UNDERLYING THE DIFFERENTIATION OF THE PEDICEL
CC ABSCISSION ZONE. MAY ALSO BE INVOLVED IN THE MAINTENANCE OF THE
CC INFLORESCENCE MERISTEM STATE.
CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -|- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN SHOOT
CC TIPS AND AXILLARY BUDS. ALSO FOUND IN FULLY DEVELOPED PEDICELS AND
CC FLOWERS.
CC -|- BIOCHEMISTRY: Mutation in 'jointless' yields 'stemless' tomato
CC fruits which are widely used in the processing tomato industry.
CC The fruits support mechanical harvesting and are not subject to
CC physical wounding during transportation.
CC -|- SIMILARITY: Contains 1 K-box dimerization domain.
CC -|- SIMILARITY: Contains 1 MADS-box domain.
CC -----
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CC -----
DR EMBL: AF275345; AAC09811.1; -.
DR HSSP: P11746; IMNM.
DR TRANSFAC: T04740; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Developmental protein;
KW Nuclear protein.
FT DOMAIN 3 57 MADS-box.
FT DOMAIN 59 173 K-box.
FT DOMAIN 58 61 POLY-SER.
FT DOMAIN 176 183 POLY-ASN.
FT DOMAIN 200 204 POLY-ASN.
SQ SEQUENCE 265 AA; 30426 MW; EB687F9D9D9C1B5D CRC64;

Query Match 30.3%; Score 334; DB 1; Length 265;
Best Local Similarity 38.1%; Pred. No. 1.7e-14;
Matches 82; Conservative 45; Mismatches 38; Indels 30; Gaps 8;

QY 1 MGRGVETIRKINSNQQVYTSKRNGIITKAKETIVLCAKVSLLIYSSSGKVEYCSF 60
DB 1 MAREKIQIKKINDSTAQVTFKRRRLGFKABELSVLCPADVALLIFSGTKLFDYSSS 60
QY 61 STLTLEILDK--YHGSGKKLMDAKHENL---SNEVDVKKDNDSMOVELRLHKGEDIT 114
DB 61 S--MKQILERRDLHSHKNEKL--DPSLELQVENSNSYRLSEKSHRLRQWRGELQ 117
QY 115 SLNHELMALAEZALNGLTSL---RDKSKFVDMWRDNGKALEDENKRLTYELQKQDEM 170
DB 118 GINIELLOQLERSLSTGLSRVIERKDKIMEINLOQKGMHLMENKLT-----RQVVM 172
QY 171 KIKENVRMNENGYHQRQLG-----NYNNNQ 195
DB 173 BISSNNNNNNNGY--REAGVVFEEPDENGFNNNNNE 205

Search completed: September 27, 2004, 09:25:44
Job time : 15.4295 secs

No.	Score	Match	Length	DB	ID	Description
1	714.5	64.8	208	12	US-10-424-599-208168	Sequence 208168
2	714.5	64.8	209	12	US-10-425-114-40799	Sequence 40799
3	660.5	59.9	208	12	US-10-412-6999-56	Sequence 56, App
4	659	59.3	207	12	US-10-424-599-175060	Sequence 175060
5	642.5	58.3	228	12	US-10-425-114-66169	Sequence 66169
6	630.5	57.2	205	12	US-10-425-114-39944	Sequence 39944
7	563	51.0	190	12	US-10-425-114-39581	Sequence 39581
8	561	50.9	190	12	US-10-425-114-40296	Sequence 40296
9	380	33.3	227	12	US-10-424-599-26366	Sequence 26366
10	367.5	33.3	260	16	US-10-437-963-113197	Sequence 113197
11	364.5	32.6	229	12	US-10-424-599-26637	Sequence 26637
12	360	32.6	149	16	US-10-767-901-39443	Sequence 39443
13	360	32.6	223	12	US-10-425-114-42492	Sequence 42492
14	358	32.5	227	12	US-10-104-580-4	Sequence 4, App
15	355.5	32.2	246	14	US-10-259-165-46	Sequence 46, App

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RESULT 1
US-10-424-599-208168
Sequence 208168, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovacic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongmei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for F
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 208168
LENGTH: 208
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
US-10-424-599-208168
PAT_MRI3847_2C.1.pdf

```

	Query Match	64.8%	Score 714.5	DB 12	Length 208
	Best Local Similarity	64.7%	Pred. No. 1,4e-54		
	Matches 139	Conservative 38	Mismatches 31	Indels 7	Gaps 3
QY	1 MGRGKVIKKRIENSSNQVTKSRKRNNIIKKAKEIITLCDAKYSLLTIYSSSGXAVEYCSP	60			
Dd	1 MGRKIKIIRKIENSSNQVTISKRRKGILLKKAKEIITLCDAQSLLIIIFASGGKHDIYSP	60			
QY	61 STTTLTEILDKYHGOSGKKLDWDAKHENISNFVDRAVKDNDMSQVELRLHKESDITSLNHVE	120			
Dd	61 STTDLIDLEYHTKSGKRLWDAKHENINGEIERLKENDSMQETLRHLKGDINDSLNYKE	120			
QY	121 LMALEELNENGGLNISIRPKQSKPFVDMARDNGKALDENKRLTYELQKQOEKIKENTAVNME	180			
Dd	121 LMALEDLLEFLGLSVREKQMDYYRMLRNDRDKILEENREINF---IMQQIAEEGAEEVD	177			

QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215
DB 178 NGFDQ-SVRDYNH--MPFAFRVQPMQPNLOERI 208

RESULT 2

US-10-425-114-40799
; Sequence 40799, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40799
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3030-006-DB_FLI.pcp
US-10-425-114-40799

Query Match 64.8%; Score 714.5; DB 12; Length 209;
Best Local Similarity 64.7%; Pred. No. 1.4e-54;
Matches 139; Conservative 38; Mismatches 31; Indels 7; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRRNGIITVLCDAKVSLLIYSSSGKWEYCSP 60
DB 2 MGRGKEIKRIENSSNRQVTSKRRNGIITVLCDAQVSLIIFASGKNHDIISP 61
QY 61 STTLEILDYKHGSGKGLMDAKHENTLSNEVDYKNDSDMQVELRLHKGEDITSLNHVE 120
DB 62 STTLDILERYHAKTSKGLMDAKHENTLNGEIRLKKENDSQILRLHKGEDINSLNKYE 121
QY 121 LMALEBALENGITSTRDKOSKFDVDMWRDNGKALEDENKRLTYELQKQOEMKIKENYRME 180
DB 122 LMALEDALETGLVSVREKQMDVYRMLRNRNDKILEENNELNF--LWQQLAEBGAREVD 178
QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215
DB 179 NGFDQ-SVRDYNH--MPFAFRVQPMQPNLOERI 208

RESULT 3

US-10-412-699B-56
; Sequence 56, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline B.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Brown, Pierre E.
; APPLICANT: Pindea, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.

APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Rogerick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 208
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G134
US-10-412-699B-56

Query Match 59.9%; Score 660.5; DB 12; Length 208;
Best Local Similarity 60.5%; Pred. No. 7.4e-50;
Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTSKRRNGIITVLCDAKVSLLIYSSSGKWEYCSP 60
DB 1 MGRGKEIKRIENSSNRQVTSKRRNGIITVLCDAKVALIIFASGKNHDIYCCP 60
QY 61 STTLEILDYKHGSGKGLMDAKHENTLSNEVDYKNDSDMQVELRLHKGEDITSLNHVE 120
DB 62 SMDLGMDQYQKLSGKGLMDAKHENTLSNEIDRIKENDSQILRLHKGEDIQSLNKN 120
QY 121 LMALEBALENGITSTRDKOSKFDVDMWRDNGKALEDENKRLTYELQKQOEMKIKENYRME 180
DB 122 LMAVERAIEHGDYKRDHQMELIISKRRNKKMAEERQLTFQLO-QQEMALASVARGM 179
QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215
DB 180 MEDHDQ-----FGYRVQPIQPNLOERI 202

RESULT 4

US-10-424-599-175060
; Sequence 175060, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175060
LENGTH: 207
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(207)
OTHER INFORMATION: unsure at all Xaa locations
OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1.pep
US-10-424-599-175060

Query Match 59.7%; Score 659; DB 12; Length 207;
Best Local Similarity 62.0%; Pred. No. 1e-49;
Matches 134; Conservative 35; Mismatches 37; Indels 10; Gaps 4;

QY 1 MGRGVEIKRIENSSNRQVYTSKRNGIIRKAKEITVLCDAKVSLLIYSSGKWEYCSP 60
DB 1 MGRGKIEIKRIENSSNRQVYTSKRNGIIRKAKEISVLCDAQVSLIIFGVSGKHHEYISP 60
QY 61 STLTLEIDKRYHQSCKLMDAKHENTLSNEVDKNDSDMOVELRHUKGEDITSINHYE 120
DB 61 STLTLDVDRYQASGKTLMDAKHENTLSNEIDRIKKENDSQIELRHUKGEDITSINYE 120
QY 121 LMALEBALENGSLTSIRDKOSKFDVDMWRDQKALEDENKRLTYELQKQEMKIKENVRN-M 179
DB 121 LMALEBALENGSLTSIRDKOSKFDVDMWRDQKALEDENKRLTYELQKQEMKIKENVRN-M 177
QY 180 ENGKHQROLGNYNNOQOIFPAFRVQPIQPNLQERI 215
DB 178 DNGFVN--EIKRVFNSHMQRAASLK---QPNLKERI 207

RESULT 5
US-10-425-114-66169
Sequence 66169, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66169
LENGTH: 228
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4606-002-H7_FLI.pep
US-10-425-114-66169

Query Match 58.3%; Score 642.5; DB 12; Length 228;
Best Local Similarity 58.2%; Pred. No. 3.2e-48;
Matches 144; Conservative 40; Mismatches 46; Indels 3; Gaps 2;
QY 1 MGRGVEIKRIENSSNRQVYTSKRNGIIRKAKEITVLCDAKVSLLIYSSGKWEYCSP 60
DB 17 MGRGKIEIKRIENSTRTQVTFKRRAGIVKARBEIGVLCDAVGVVIFSSGCKLVDYDSP 76
QY 61 STLTLEIDKRYHQSCKLMDAKHENTLSNEVDKNDSDMOVELRHUKGEDITSINHYE 120
DB 77 RUSLSRIIEKIQNSKIIIMGEKRLSALIDRVKKNENMOIQRLHLEGEDLNLQPRE 136
QY 121 LMALEBALENGSLTSIRDKOSKFDVDMWRDQKALEDENKRLTYELQKQEMKIKENVRN-M 180

DB 137 LIAIEBQLQNGQTMREKQMDYWRMHKTNKXMLEDEKILTFRMH-QQAVDSGKMELE 195
QY 181 NGYHQRQLGNYNNOQOIFPAFRVQPIQPNLQOE 213
DB 196 TGXYHQVQ--HBRDFISQMPFTFRVQPNHPTLQOE 226

RESULT 6
US-10-425-114-39944
Sequence 39944, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39944
LENGTH: 205
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700903463_FLI.pep
US-10-425-114-39944

Query Match 57.2%; Score 630.5; DB 12; Length 205;
Best Local Similarity 68.7%; Pred. No. 3.1e-47;
Matches 123; Conservative 26; Mismatches 27; Indels 3; Gaps 1;

QY 1 MGRGVEIKRIENSSNRQVYTSKRNGIIRKAKEITVLCDAKVSLLIYSSGKWEYCSP 60
DB 25 MGRGKIEIKRIENSSNRQVYTSKRNGIIRKAKEISVLCDAQVSLIIFGVSGKHHEYISP 84
QY 61 STLTLEIDKRYHQSCKLMDAKHENTLSNEVDKNDSDMOVELRHUKGEDITSINHYE 120
DB 85 STLTLDVDRYQASGKTLMDAKHENTLSNEIDRIKKENDSQIELRHUKGEDITSINYE 144
QY 121 LMALEBALENGSLTSIRDKOSKFDVDMWRDQKALEDENKRLTYELQKQEMKIKENVRN-M 179
DB 145 LMALEBALENGSLTSIRDKOSKFDVDMWRDQKALEDENKRLTYELQKQEMKIKENVRN-M 200

RESULT 7
US-10-425-114-39581
Sequence 39581, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39581
LENGTH: 190
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700382572_FLI.pep
US-10-425-114-39581

```

QY      120  ELMALBEALENGITSIRDKOSKFVDMRDNCK---ALBENKRLTYELOQOEMKIKEN 175
          ::  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Nb      121  DINDLEOLEFSFSTKYVARKHOLNOLNDRKREHLEONSFL----- 165

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```
QY 176 VANNENGYHQRQLGN-----YNNNOQQI:PF----- 200
DB 166 CEMINENHHQAAGVGGDDVAKAVEMAPVLSMLTAPAYVGBESSATLQUTPLHVAADAA 225
QY 201 --AFRVQPIQPNLQ 213
DB 226 AAGFRLQPTQPNLQD 240

RESULT 11
US-10-424-599-263637
; Sequence 263637, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 265684
; SEQ ID NO 263637
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pep
US-10-424-599-263637

Query Match 33.0%; Score 364.5; DB 12; Length 234;
Best Local Similarity 33.9%; Pred. No. 7.7e-24;
Matches 78; Conservative 51; Mismatches 72; Indels 29; Gaps 4;

QY 1 MARGKEIKRIENSSNRQVTSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKXVEYCSPTL 60
DB 1 MARGKIQIKRIENTNRQVTSKRRNGLFKCANELTVLCDAKVSLLIYSSSGKXHEITSP 60
QY 61 STTLTEILDKYHGSGSKLMDAKHENLSNEVDVKKNDNSQVLELRLHKGEDITSLNHVE 120
DB 61 STSKQFPDQYQMTLGVDLNMSHYEMQENLKKLKDVRNMLRKEIRORXGDCIANDLGEMD 120
QY 121 LMALFEALENGLTSIRDKSKFVDMKRDNGKALDEENKRLTYELQKO-QEMKIKENVAN- 178
DB 121 LKLEEMDKAAKVAVERSC-----KTRERQKQKVTIRIVYORKKFNNEKEVHR 170
QY 179 -----MENGYHQRQLGNYNNOQQI:PF:AFRVQPIQPNLQ 212
DB 171 LURDLARADPRFALIDNGEYESVIGPSNLGPRM-FALSLQPSHPSAQ 219

RESULT 12
US-10-767-701-39443
; Sequence 39443, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39443
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
```

```
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1852_1.pep
US-10-767-701-39443

Query Match 32.6%; Score 360; DB 16; Length 149;
Best Local Similarity 49.0%; Pred. No. 1e-23;
Matches 73; Conservative 29; Mismatches 39; Indels 8; Gaps 3;

QY 66 EILDKXHGSGSKLMDAKHENLSNEVDVKKNDNSQVLELRLHKGEDITSLNHVEIMALE 125
DB 6 KILEKQYQNSGKILMDKSKLSAIDRIKIKENDTQIEIRLHKGEDINSLOPKDLIMIE 65
QY 126 EALENGLTSIRDKSKFVDMKRDNGKALDEENKRLTYELQKOQEMKIKENVANMENGYH- 184
DB 66 EALDNGLTQNEKLMKEMWERRVANNKXMEDEKTLAFKJH-QQDIALSGSMRELEJGTHP 124
QY 185 QROLGNNNNQQOIPFAFRVQPIQPNLQ 213
DB 125 DRDLA-----AQMPITFRVQPSHPNLQD 147

RESULT 13
US-10-425-114-42492
; Sequence 42492, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K.
; APPLICANT: Screen Steven E
; APPLICANT: Tabaska Jack E
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42492
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700958586_FLI.pep
US-10-425-114-42492

Query Match 32.6%; Score 360; DB 12; Length 223;
Best Local Similarity 36.3%; Pred. No. 1.8e-23;
Matches 77; Conservative 49; Mismatches 78; Indels 8; Gaps 3;

QY 5 KVEIKRIENSSNRQVTSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKXVEYCSPTL 64
DB 1 KIQIKRIENTNRQVTSKRRNGLFKCANELTVLCDAKVSLLIYSSSGKXHEITSP 60
QY 65 TELDKYHGSGSKLMDAKHENLSNEVDVKKNDNSQVLELRLHKGEDITSLNHVEIMALE 124
DB 61 KQFPDQYQMTLGVDLNMSHYEMQENLKKLKDVRNMLRKEIRORXGDCIANDLGEMD 120
QY 125 EALENGLTSIRDKSKF-----VDMKRDNGKALDEENKRLTYELQKOQEMKIKENVANME 180
DB 121 EEMDKAAKVAVERKQVITNQIDTQKCKFNNEKEVANRLRLDLDAAE--DPRFALID 177
QY 181 NGYHQRQLGNYNNOQQI:PF:AFRVQPIQPNLQ 212
DB 178 NGGEYESVIGPSNLGPRM-FALSLQPSHPSAQ 208

RESULT 14
US-10-104-580-4
; Sequence 4, Application US/10104580
; Publication No. US2003003628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:19:49 / Search time 24.0492 Seconds
(without alignments)
859,952 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGVEIKRIENSSNRQVT.....QQIPFAFVQPIQPNLOERI 215

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 78:***
2: PIR:***
3: PIR:***
4: PIR:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	740.5	67.1	212	2	S31707	floral homeotic pr
2	739.5	67.0	212	2	S60288	FBP3 protein gar
3	713	64.6	215	2	S28062	homeotic protein g
4	707	64.1	209	2	S35226	homeotic protein g
5	684.5	62.1	210	2	U01689	floral binding pro
6	660.5	59.9	208	2	A53839	B function floral
7	620.5	56.3	210	2	T03902	MADS4 box protein
8	617	55.9	209	2	T03894	MADS box protein -
9	411	37.3	222	2	S23731	MADS box protein T
10	377.5	34.5	229	2	T09335	MADS-box protein N
11	377.5	34.2	231	2	S31693	MADS box protein g
12	367.5	33.3	224	2	T14474	MADS box protein 2
13	360	32.6	228	2	T07066	MADS-box protein h
14	359	32.5	228	2	T07410	MADS box protein h
15	356.5	32.3	232	2	A42095	floral homeotic pr
16	349	31.6	227	2	S12378	MADS box protein d
17	346	31.4	273	2	T03410	MADS box protein -
18	343.5	31.1	224	2	T14474	MADS box protein a
19	335	30.4	251	2	T00656	MADS box protein A
20	334.5	30.3	243	2	S71756	MADS box protein D
21	334	30.3	248	2	B39534	MADS box protein A
22	332	30.1	214	2	T10715	MADS-box protein C
23	332	30.1	247	2	T06843	MADS-box protein -
24	331	30.0	261	2	T09603	MADS-box protein 3
25	330	29.9	242	2	S71208	MADS box protein A
26	329	29.8	242	2	T10467	MADS box protein D
27	327.5	29.7	245	2	T09569	MADS box protein M
28	327.5	29.7	252	2	T51409	MADS box protein A
29	326.5	29.6	258	2	S57793	MADS box protein A

30	326	29.6	261	2	S51935	probable MADS-box
31	325	29.5	228	2	T14737	MADS box protein -
32	324	29.4	242	2	T10486	MADS box protein M
33	324	29.4	242	2	T09571	MADS box protein l
34	323.5	29.3	220	2	T51827	MADS-box protein A
35	323.5	29.3	220	2	T05580	MADS-box protein h
36	323.5	29.3	250	2	T07100	MADS box protein 1
37	321.5	29.1	246	2	T17023	MADS box protein pr
38	320.5	29.1	248	2	A39534	floral homeotic pr
39	319.5	29.0	246	2	E39574	floral homeotic pr
40	319.5	29.0	258	2	G84858	floral homeodomain
41	319	28.9	284	2	T05033	floral homeotic pr
42	319	28.9	284	2	A85214	floral homeotic pr
43	318.5	28.9	247	2	S78015	MADS box protein D
44	318	28.8	253	2	S73586	MADS box protein a
45	318	28.8	254	2	S52236	MADS box protein a

ALIGNMENTS

RESULT 1
S31707
floral homeotic protein pmas2 - garden petunia
N/Alternate names: MADS box-containing protein; transcription factor pmas2
C/Species: Petunia x hybrida (garden petunia)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Dec-1999
C/Accession: S31707
R/Kush, A.; Brunelle, A.; Shevell, D.; Chua, N.H.
submitted to the EMBL Data Library, November 1992
A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box
A/Reference number: S31693
A/Accession: S31707
A/Molecule type: mRNA
A/Residues: 1-212 (KUS)
A/Cross-references: EMBL: X69947; NID: G22666; PID: G22667
A/Suprafamily: transcription factor squa; serum response factor DNA-binding domain homo;
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
P/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 67.1%; Score 740.5; DB 2; Length 212;
Best Local Similarity 67.4%; Pred. No. 8.3e-41;
Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY	1	MGRGVEIKRIENSSNRQVTYSKRNGLIKKAKETIVCDKAVSLIYSSGKWEYCSP	60
DB	1	MGRGVEIKRIENSSNRQVTYSKRNGLIKKAKETIVCDKAVSLIYSSGKWEYCSP	60
QY	61	STTLEIIDKTHGSGGKLMADAKHENSNEVDYVKNDNQVLRHAKGDIYSLNIVE	120
DB	61	STTLEIIDKTHGSGGKLMADAKHENSNEVDYVKNDNQVLRHAKGDIYSLNIVE	120
QY	121	LMALFEALENGTLTIRDSKSKFVDMWRDNGKALJEDENRLTYELOQOEMKIKENVRNME	180
DB	121	LMALFEALENGTLTIRDSKSKFVDMWRDNGKALJEDENRLTYELOQOEMKIKENVRNME	180
QY	181	NGYHQRQAGNNNNNOQIPFAFVQPIQPNLOERI	215
DB	181	NGYHQRQAGNNNNNOQIPFAFVQPIQPNLOERI	215
QY	181	EYVHOR---DRDYEQWPFALRVQPMQPNLHERM	212
DB	181	EYVHOR---DRDYEQWPFALRVQPMQPNLHERM	212

RESULT 2
S60288
FBP3 protein - garden petunia
C/Species: Petunia x hybrida (garden petunia)
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C/Accession: S60288
R/Angeles, G.C.; Franken, J.; Busscher, M.; Weiss, D.; van Tunen, A.J.
Plant J. 5, 33-44, 1994
A/Title: Co-suppression of the petunia homeotic gene fbp3 affects the identity of the g
A/Reference number: S60288; NCID: 94177174; PMID: 7907515
A/Accession: S60288
A/Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-212 <ANG>
 A:Cross-references: EMBL:X71417; NID:9454264; PIDN:CAA50549.1; PID:9454265
 C:Species: *Antirrhinum majus* (garden snapdragon)
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 67.0%; Score 739.5; DB 2; Length 212;
 Best Local Similarity 67.4%; Pred. No. 9.6e-41;
 Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 DB 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 QY 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 DB 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 DB 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPIDPNIQER 215
 DB 181 EVYHQR---DRDYEQQMPFALRVQPMQENLHERM 212

RESULT 3

S28062
 homeotic protein globosa - garden snapdragon
 C:Species: *Antirrhinum majus* (garden snapdragon)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
 C:Accession: S28062
 R:Prodbner, W.; Ramirez, L.; Morte, P.; Hue, I.; Huisser, P.; Loemig, W.F.; Saedler, H.
 EMBO J. 11, 4693-4704, 1992
 A:Title: GLOBOSA: a homeotic gene which interacts with DEFICIENS in the control of Antirrhinum
 A:Reference number: S28062; MUID:9309942; PMID:1361166
 A:Accession type: DNA
 A:Residues: 1-215 <TRO>
 A:Cross-references: EMBL:X68831; NID:g16023; PIDN:CAA48725.1; PID:g16024
 A:Gene: glo
 A:Introns: 63/2; 85/3; 106/2; 139/3; 149/3; 164/3
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; nucleus; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 64.6%; Score 713; DB 2; Length 215;
 Best Local Similarity 63.1%; Pred. No. 4.9e-39;
 Matches 135; Conservative 40; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 DB 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 QY 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 DB 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 DB 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPIDPNIQER 214
 DB 181 AVYDHHHONLADYEAQVFAFRVOPIDPNIQER 214

RESULT 4

S35226
 homeotic protein globosa homolog - common tobacco
 C:Species: *Nicotiana tabacum* (common tobacco)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
 C:Accession: S35226; S31360
 R:Hansen, G.; Estruch, J.J.; Sommer, H.; Spena, A.
 Mol. Gen. Genet. 239, 310-312, 1993
 A:Title: NGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of *Antirrhinum m*
 A:Reference number: S35226; MUID:93288002; PMID:8099711
 A:Accession: S35226
 A:Molecule type: mRNA
 A:Residues: 1-209 <HAN>
 A:Cross-references: EMBL:X67959; NID:g19870; PIDN:CAA48142.1; PID:g19871
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; nucleus; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 64.1%; Score 707; DB 2; Length 209;
 Best Local Similarity 63.6%; Pred. No. 1.2e-38;
 Matches 136; Conservative 41; Mismatches 31; Indels 6; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 DB 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 QY 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 DB 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 DB 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPIDPNIQER 214
 DB 179 EVYHQR---NEYOTQMPFAFRVOPIDPNIQER 208

RESULT 5

JQ1689
 floral binding protein 1 - garden petunia
 C:Species: *Petunia x hybrida* (garden petunia)
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000
 C:Accession: JQ1689
 R:Aggenent, G.C.; Busscher, M.; Franken, J.; Mol, J.N.M.; van Tunen, A.J.
 Plant Cell 4, 983-993, 1992
 A:Title: Differential expression of two MADS box genes in wild-type and mutant *Petunia fr*
 A:Reference number: JQ1689; MUID:9300537; PMID:1356537
 A:Accession: JQ1689
 A:Molecule type: mRNA
 A:Residues: 1-210 <ANG>
 A:Cross-references: GB:M91190; NID:g169253; PIDN:AAA3731.1; PID:g169254
 A:Experimental source: flower
 A:Gene: fbpl

A:Introns: 61/3; 83/3; 104/3; 137/3; 147/1; 162/3
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; nucleus; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 62.1%; Score 684.5; DB 2; Length 210;
 Best Local Similarity 62.3%; Pred. No. 3.2e-37;
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 DB 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYECSP 60
 QY 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 DB 61 STLTLEIDKXHGQSGKGLMDAKHENTLSNEVDKVKNDNSQVLELRLHKGEDITSLNHVE 120
 QY 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 DB 121 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 180
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPIDPNIQER 214
 DB 119 LMALEALENGTLTIRDSKSFVDMRDNGKALDENKRLTYELQKQGEKIKENVRNME 178

QY 181 NGYHQRQLGNVNNQOQIPFAFRVQPIQPNLOE 215
 DB 179 EVFOQRENDHYONH---MFAFRVQPMQPNLOE 210

RESULT 6

Accession: A53839
 B function: floral homeotic protein PI - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
 C:Accession: A53839
 R:Goto, K.; Meyerowitz, E.M.
 Genes Dev. 8, 1548-1560, 1994
 A:Title: Function and regulation of the Arabidopsis floral homeotic gene PISTILLATA.
 A:Reference number: A53839; PMID:95047314; PMID:7958839
 A:Accession: A53839
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-208 <GOT>
 A:Cross-references: GB:DJ0807; NID:9642128; PIDN:BA06465.1; PID:9493620
 C:Gene: PI
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: homeobox
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 59.9%; Score 660.5; DB 2; Length 208;
 Best Local Similarity 60.5%; Pred. No. 1.1e-35; Indels 13; Gaps 2;
 Matches 10; Conservative 33; Mismatches 39;

QY 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60
 DB 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKNDNSQVLELRHKGEDITSLNHYE 120
 DB 61 SMDLGMLDQYQYLSKSKLMDAKHENTLSNEVDYKNDNSQVLELRHKGEDITSLNHYE 120
 QY 121 LMALEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 DB 121 LMAVEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 QY 181 NGYHQRQLGNVNNQOQIPFAFRVQPIQPNLOE 215
 DB 181 NGYHQRQLGNVNNQOQIPFAFRVQPIQPNLOE 215
 DB 180 MRDHDGQ-----FGYRVCPIQPNLOE 202

RESULT 7

Accession: T03902
 MADS4 box protein - rice
 C:Species: Oryza sativa (rice)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Dec-1999
 C:Accession: T03902
 R:Chung, Y.Y.; Kim, S.R.; Kang, H.G.; Noh, Y.S.; Park, M.C.; Finkel, D.; An, G.
 Plant Sci. 109, 45-56, 1995
 A:Title: Characterization of two rice MADS box genes homologous to GLOBOSA.
 A:Reference number: Z15129
 A:Accession: T03902
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-210 <CHU>
 A:Cross-references: EMBL:LJ37527; NID:92961436; PIDN:AA05723.1; PID:92961437
 A:Experimental source: flower
 C:Gene: MADS4
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 56.3%; Score 620.5; DB 2; Length 210;
 Best Local Similarity 55.9%; Pred. No. 4.1e-33; Indels 5; Gaps 2;
 Matches 119; Conservative 41; Mismatches 48;

QY 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60

DB 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKNDNSQVLELRHKGEDITSLNHYE 120
 DB 61 KTLISRLIEKYQTSNGKILMDERKSLSAEIDVKKENDVQLELRHKGEDITSLNHYE 120
 QY 121 LMALEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 DB 121 LMALEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 QY 181 NGYHQRQLGNVNNQOQIPFAFRVQPIQPNLOE 213
 DB 180 LGYHNR-----DDRDPAASMPFTFRVQPSHPNLOE 208

RESULT 8

Accession: T03894
 MADS box protein - rice
 C:Species: Oryza sativa (rice)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Dec-1999
 C:Accession: T03894
 R:Chung, Y.Y.; Kim, S.R.; Kang, H.G.; Noh, Y.S.; Park, M.C.; Finkel, D.; An, G.
 Plant Sci. 109, 45-56, 1995
 A:Title: Characterization of two rice MADS box genes homologous to GLOBOSA.
 A:Reference number: Z15129
 A:Accession: T03894
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-209 <CHU>
 A:Cross-references: EMBL:LJ37526; NID:9886400; PIDN:AA52709.1; PID:9886401
 A:Experimental source: flower
 C:Gene: MADS2
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 55.9%; Score 617; DB 2; Length 209;
 Best Local Similarity 55.4%; Pred. No. 6.9e-33; Indels 6; Gaps 2;
 Matches 118; Conservative 44; Mismatches 45;

QY 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60
 DB 1 MGRGKIEIKRIENSNROVYTSKRNGIIRKAKETITVLCDAKVSLLIYSSSGKMYEYCS 60
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKNDNSQVLELRHKGEDITSLNHYE 120
 DB 61 KTLISRLIEKYQTSNGKILMDERKSLSAEIDVKKENDVQLELRHKGEDITSLNHYE 120
 QY 121 LMALEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 DB 121 LMALEALENLGLTIRDKOSKFDVMDRNGKALEDENKRLTYELQKQEMKIKENYANNE 180
 QY 181 NGYHQRQLGNVNNQOQIPFAFRVQPIQPNLOE 213
 DB 180 LGYHNR-----DFAAQWPIFRVQPSHPNLOE 207

RESULT 9

Accession: S23731
 MADS box protein TDR6 - tomato (fragment)
 N:Alternate names: floral homeotic protein TM6
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 27-May-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1999
 R:Phnuit, L.; Abu-Abed, W.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E.
 Plant J. 1, 255-266, 1991
 A:Title: The MADS box gene family in tomato: temporal expression during floral developm
 A:Reference number: S23728; PMID:93251098; PMID:1688249
 A:Accession: S23731
 A:Molecule type: mRNA
 A:Residues: 1-222 <PNU>
 A:Cross-references: EMBL:X60759

R:Pruett, L.
submitted to the EMBL Data Library, July 1991

A/Reference number: S38778

A/Accession: S38778

A/Molecule type: mRNA

A/Residues: 1-159, 'T', 161-222 <PNF>

A/Cross-references: EMBL:X60759; NID:g19385; PDB:g19386

C/Genetics:

A/Map position: 2

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>

Query Match 37.3%; Score 411; DB 2; Length 222;
Best Local Similarity 41.3%; Pred. No. 1.2e-19;

Matches 88; Conservative 43; Mismatches 74; Indels 8; Gaps 4;

QY 4 GATGKRIKRNSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKMYECSPET 63

DB 1 GRIEIKRIENSTNRQVTSKRNGIFKKEKELTVLCDAKISLIMLSIRKYEYTSPTT 60

QY 64 LTELIDKRYHGSQSKLMDAKHENLSNEVDKVKDMSQVEIRHLKGEDITSLNHVELMA 123

DB 61 TKKMDIQYOSALGVDMISIHFKQOENLTKLKEINNKLRREIRQRTGDMGSLMDQLCH 120

QY 124 LEEALENGTLSTIRDSKSFV---DMRDNGKALDEENKRLTYELQKQOENKIKENVRNM 179

DB 121 LOENTITESVAEIRERKHYIKQDTCKKAKANLEQGNIVLDEAKCE-DPKYGVEN 179

QY 180 ENGYNOROLGNVNNNQOIPFAFRVQPIQPNQ 212

DB 180 EGHYSAVA--FANGVHNL-YAFRLQPLHPNQ 209

RESULT 10

T09335

MADS-box protein NMH 7 - alfalfa

C/Species: Medicago sativa (alfalfa)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Dec-1999

C/Accession: T09335

R/Kirby, C.; Heard, J.; Carroll, S.; Lesher, J.; Ganter, G.; Dunn, K.

A/Reference number: 216647

A/Accession: T09335

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-229 <KIR>

A/Cross-references: EMBL:AF042068; NID:g2827299; PDB:g2827300

A/Experimental source: strain Iroquois; root nodules

C/Genetics:

A/Gene: nmh 7

A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 34.5%; Score 381; DB 2; Length 229;
Best Local Similarity 37.9%; Pred. No. 1.1e-17;

Matches 81; Conservative 47; Mismatches 78; Indels 8; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKMYECSP 60

DB 1 MARGKIQRIENTNRQVTSKRNGIFKAKNELTVLCDAKVSIIIMFSITGLKHEYIS 60

QY 61 STTLTEILDKRYHGSQSKLMDAKHENLSNEVDKVKDMSQVEIRHLKGEDITSLNHVE 120

DB 61 SASTKQFPDQYQMTVGIDLVNSHYENQENIKKLKDVNRNLKREIRQMGECNDLSMER 120

QY 121 LMALEALENGTLSTIRDSKSFV---VDMRDNGKALDEENKRLTYELQKQOENKIKENVR 176

DB 121 LRLLEDEMDKAKAKIRERKHYIKQDTCKKAKANLEQGNIVLDEAKCE---DPRP 177

QY 177 RNENGYNOROLGNVNNNQOIPFAFRVQPIQPN 210

DB 178 EMDNDGSEYEVIGFISNLGPRM-FALSLOPTHPN 210

RESULT 11

S31693

MADS box protein gp - garden petunia

N/Alternate names: floral homeotic protein gp; transcription factor gp

C/Species: Petunia x hybrida (garden petunia)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999

C/Accession: S31693

R/Kush, A.; Brunelle, A.; Shevell, D.; Chu, N.H.

submitted to the EMBL Data Library, November 1992

A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box

A/Reference number: S31693

A/Accession: S31693

A/Molecule type: mRNA

A/Residues: 1-231 <KUS>

A/Cross-references: EMBL:X69946; NID:g22664; PDB:g22665

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 34.2%; Score 377.5; DB 2; Length 231;
Best Local Similarity 38.5%; Pred. No. 1.8e-17;

Matches 84; Conservative 47; Mismatches 72; Indels 15; Gaps 4;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKMYECSP 60

DB 1 MARGKIQRIENQVTSKRNGIFKAKNELTVLCDAKVSIIIMFSITGLKHEYIS 60

QY 61 STTLTEILDKRYHGSQSKLMDAKHENLSNEVDKVKDMSQVEIRHLKGEDITSLNHVE 120

DB 61 SITTKQLPDYQKTVGVDMISIHFKQOENLTKLKEINNKLRREIRQRTGDMGSLMDQLCH 120

QY 121 LMALEALENGTLSTIRDSKSFVDMRDNGKALDEENKRLTYELQKQOENKIKENVRNM 180

DB 121 LEELEMDVNSLKLIRERKHYIKQDTCKKAKANLEQGNIVLDEAKCE---DPRP 174

QY 181 NGYHROLGNVNNNQOIPFAFRVQPIQPN 210

DB 175 PGLVDEQBDVNSVGLFPRGHRILALRLQGNHHPN 211

RESULT 12

T14473

MADS box protein 2AP3 - broccoli

N/Alternate names: homeotic protein 2AP3

C/Species: Brassica oleracea var. botrytis (broccoli)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C/Accession: T14473

R/Carr, S.M.; Irish, V.F.

Planta 201, 179-188, 1997

A/Title: Floral homeotic gene expression defines developmental arrest stages in Brassica

A/Reference number: 218110; MUID:97237761; PMID:9084216

A/Accession: T14473

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-224 <CAR>

A/Cross-references: EMBL:U67455; NID:g1561785; PDB:g1561786

A/Experimental source: variety Italica; flower

C/Genetics:

A/Gene: 2AP3

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 33.3%; Score 367.5; DB 2; Length 224;
Best Local Similarity 37.1%; Pred. No. 7.6e-17;

Matches 78; Conservative 47; Mismatches 66; Indels 19; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKMYECSP 60

DB 1 MARGKIQRIENQVTSKRNGIFKAKNELTVLCDAKVSIIIMFSITGLKHEYIS 60

RESULT 15
 A42095
 floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C/Accession: A42095; S52533; T47593
 R/Jack, T.; Brockman, L.T.; Meyerowitz, E.M.
 J11 68, 683-697, 1992
 A>Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is expressed in floral meristems
 A/Reference number: A42095; MUID:92154682; PMID:1346756
 A/Accession: A42095
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-232 <UAC>
 A/Cross-References: GB:M66357; NID:g166607; PIDN:AAA32740.1; PID:g166608
 A/Experimental source: petals, stamens
 A/Note: sequence extracted from NCBI Backbone (NCBIN:82520, NCBIT:82521)
 R/Okanoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
 Plant Mol. Biol. 26, 465-472, 1994
 A>Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis
 A/Reference number: S52633; MUID:95036018; PMID:7948893
 A/Accession: S52633
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-63 <OKA>
 A/Cross-References: GB:D21125
 R/Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quettler, F.; Salanoubat M.Mewes
 submitted to the Protein Sequence Database, March 2000
 A/Reference number: Z24469
 A/Accession: T47593
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-232 <BLO>
 A/Cross-References: EMBL:AL132971
 A/Experimental source: cultivar Columbia; BAC clone T12E18
 C/Genetics:
 A/Map position: 3
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 A/Note: T12E18.10
 C/Suprafamily: DNA transcription factor squa; serum response factor DNA-binding domain homo
 C/Keywords: DNA binding; nucleus; transcription regulation
 F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 32.3%; Score 356.5; DB 2; Length 232;
 Best Local Similarity 35.1%; Pred. No. 4e-16;
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OW nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:22:22 ; Search time 76.0087 Seconds
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Title: US-10-069-527-1
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Searched: 682709 seqs, 277475446 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	31	3.6	1246	4 US-09-336-643A-28	Sequence 28, Appl
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7	30	3.5	572	4 US-09-342-653-5	Sequence 5, Appl
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9	30	3.5	1080	2 US-08-722-050-1	Sequence 1, Appl
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C 36	29	3.3	840	4 US-09-244-111-5	Sequence 5, Appl
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171	28	3.2	1747	4	US-08-888-818C-1	Sequence 1, Appl	244	28	3.2				
172	28	3.2	1798	4	US-09-797-906-1	Sequence 46, Appl	245	28	3.2				
173	28	3.2	1801	4	US-09-336-536-46	Sequence 46, Appl	246	28	3.2				

247	28	3.2	3134	4	US-09-183-861-1	Sequence 1, Appli	320	27	3.1	72	4	US-09-621-976-12390	Sequence 12390, A
248	28	3.2	3134	4	US-09-022-765-1	Sequence 1, Appli	321	27	3.1	73	4	US-09-621-976-14698	Sequence 14698, A
249	28	3.2	3134	4	US-09-551-974A-1	Sequence 1, Appli	322	27	3.1	77	4	US-09-621-976-12266	Sequence 12266, A
250	28	3.2	3134	4	US-09-565-501A-1	Sequence 1, Appli	323	27	3.1	81	3	US-09-014-616-57	Sequence 57, Appli
251	28	3.2	3134	4	US-09-639-206A-1	Sequence 1, Appli	324	27	3.1	81	4	US-09-621-976-12198	Sequence 12198, A
252	28	3.2	3134	4	US-09-874-923-1	Sequence 1, Appli	325	27	3.1	81	4	US-09-621-976-13601	Sequence 13601, A
253	28	3.2	3207	1	US-07-946-427-1	Sequence 1, Appli	326	27	3.1	82	4	US-09-621-976-11849	Sequence 11849, A
254	28	3.2	3207	1	US-08-483-322-1	Sequence 1, Appli	327	27	3.1	82	4	US-09-621-976-11441	Sequence 11841, A
255	28	3.2	3207	2	US-08-478-882-1	Sequence 1, Appli	328	27	3.1	82	4	US-09-621-976-11864	Sequence 11864, A
256	28	3.2	3319	3	US-08-335-844A-15	Sequence 15, Appli	329	27	3.1	82	4	US-09-621-976-11868	Sequence 11868, A
257	28	3.2	3319	4	US-09-129-365-15	Sequence 15, Appli	330	27	3.1	82	4	US-09-621-976-11944	Sequence 11944, A
258	28	3.2	3383	4	US-09-130-491-3	Sequence 3, Appli	331	27	3.1	82	4	US-09-621-976-11849	Sequence 11849, A
259	28	3.2	3383	1	US-08-252-626A-1	Sequence 1, Appli	332	27	3.1	82	4	US-09-621-976-12015	Sequence 12015, A
260	28	3.2	3652	4	US-08-936-135-5	Sequence 5, Appli	333	27	3.1	82	4	US-09-621-976-12088	Sequence 12088, A
261	28	3.2	3652	4	US-09-439-711C-5	Sequence 5, Appli	334	27	3.1	82	4	US-09-621-976-12103	Sequence 12103, A
262	28	3.2	3695	1	US-08-091-569-1	Sequence 1, Appli	335	27	3.1	82	4	US-09-621-976-12127	Sequence 12127, A
263	28	3.2	3695	1	US-08-203-676-1	Sequence 1, Appli	336	27	3.1	82	4	US-09-621-976-12131	Sequence 12131, A
264	28	3.2	3695	2	US-08-822-238-1	Sequence 1, Appli	337	27	3.1	82	4	US-09-621-976-12137	Sequence 12137, A
265	28	3.2	3736	2	US-08-480-473B-1	Sequence 1, Appli	338	27	3.1	82	4	US-09-621-976-12322	Sequence 12322, A
266	28	3.2	3736	2	US-08-915-213-1	Sequence 1, Appli	339	27	3.1	82	4	US-09-621-976-12368	Sequence 12368, A
267	28	3.2	3736	3	US-09-148-547-1	Sequence 1, Appli	340	27	3.1	82	4	US-09-621-976-13349	Sequence 13349, A
268	28	3.2	3736	3	US-09-235-217-1	Sequence 1, Appli	341	27	3.1	82	4	US-09-621-976-13526	Sequence 13526, A
269	28	3.2	3736	5	US-09-383-581-1	Sequence 1, Appli	342	27	3.1	83	4	US-09-621-976-12175	Sequence 12087, A
270	28	3.2	3736	5	US-09-121-321-15	Sequence 15, Appli	343	27	3.1	83	4	US-09-621-976-12175	Sequence 12175, A
271	28	3.2	3777	3	US-08-933-803A-15	Sequence 15, Appli	344	27	3.1	83	4	US-09-621-976-12195	Sequence 12195, A
272	28	3.2	3777	3	US-09-389-956-1	Sequence 1, Appli	345	27	3.1	83	4	US-09-621-976-12429	Sequence 12429, A
273	28	3.2	3902	4	US-09-351-224E-9	Sequence 9, Appli	346	27	3.1	84	4	US-09-621-976-12450	Sequence 12450, A
274	28	3.2	3999	4	US-09-677-682B-9	Sequence 9, Appli	347	27	3.1	84	4	US-09-621-976-12450	Sequence 11710, A
275	28	3.2	3999	4	US-09-677-682B-9	Sequence 9, Appli	348	27	3.1	85	1	US-08-478-675-97	Sequence 97, Appli
276	28	3.2	4104	1	US-07-998-003A-94	Sequence 94, Appli	349	27	3.1	85	1	US-08-677-944-1	Sequence 1, Appli
277	28	3.2	4104	1	US-08-453-274B-94	Sequence 94, Appli	350	27	3.1	90	1	US-08-677-944-2	Sequence 2, Appli
278	28	3.2	4104	1	US-08-453-695A-94	Sequence 94, Appli	351	27	3.1	90	3	US-09-254-048A-1	Sequence 1, Appli
279	28	3.2	4104	1	US-08-268-161A-94	Sequence 94, Appli	352	27	3.1	90	3	US-09-921-203-1	Sequence 1, Appli
280	28	3.2	4104	2	US-08-455-702A-94	Sequence 94, Appli	353	27	3.1	90	4	US-09-816-089E-2	Sequence 2, Appli
281	28	3.2	4104	2	US-09-059-639-94	Sequence 94, Appli	354	27	3.1	90	4	US-09-621-976-9330	Sequence 9330, Ap
282	28	3.2	4104	5	US-09-199-780-2	Sequence 94, Appli	355	27	3.1	91	4	US-09-621-976-12161	Sequence 12161, A
283	28	3.2	4104	5	US-08-199-780-2	Sequence 2, Appli	356	27	3.1	92	4	US-09-621-976-12161	Sequence 12161, A
284	28	3.2	4104	5	US-08-316-650-2	Sequence 2, Appli	357	27	3.1	97	1	US-08-120-827-87	Sequence 87, Appli
285	28	3.2	4104	5	US-08-476-062A-52	Sequence 52, Appli	358	27	3.1	97	1	US-08-476-062A-52	Sequence 87, Appli
286	28	3.2	4704	4	US-09-023-655-1358	Sequence 1358, Ap	359	27	3.1	98	4	US-09-621-976-11444	Sequence 11744, A
287	28	3.2	4704	4	US-09-392-184-1	Sequence 1, Appli	360	27	3.1	105	2	US-08-735-381-2	Sequence 2, Appli
288	28	3.2	4704	4	US-09-705-872-2	Sequence 2, Appli	361	27	3.1	105	3	US-09-201-674-2	Sequence 1, Appli
289	28	3.2	4858	4	US-09-356-952-12	Sequence 12, Appli	362	27	3.1	105	3	US-09-621-976-13620	Sequence 13620, A
290	28	3.2	5872	4	US-08-724-394A-20	Sequence 20, Appli	363	27	3.1	106	4	US-09-621-976-12079	Sequence 12079, A
291	28	3.2	5872	4	US-08-724-394A-21	Sequence 21, Appli	364	27	3.1	106	4	US-09-621-976-12330	Sequence 12330, A
292	28	3.2	5872	4	US-09-244-794A-11	Sequence 11, Appli	365	27	3.1	106	4	US-09-621-976-12330	Sequence 59, Appli
293	28	3.2	5872	4	US-09-244-794A-12	Sequence 12, Appli	366	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
294	28	3.2	5872	4	US-09-244-794A-13	Sequence 13, Appli	367	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
295	28	3.2	5872	4	US-09-244-794A-14	Sequence 14, Appli	368	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
296	28	3.2	5872	4	US-09-244-794A-15	Sequence 15, Appli	369	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
297	28	3.2	5872	4	US-09-244-794A-16	Sequence 16, Appli	370	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
298	28	3.2	5872	4	US-09-244-794A-17	Sequence 17, Appli	371	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
299	28	3.2	5872	4	US-09-244-794A-18	Sequence 18, Appli	372	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
300	28	3.2	5872	4	US-09-244-794A-19	Sequence 19, Appli	373	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
301	28	3.2	5872	4	US-09-244-794A-20	Sequence 20, Appli	374	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
302	28	3.2	5872	4	US-09-244-794A-21	Sequence 21, Appli	375	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
303	28	3.2	5872	4	US-09-244-794A-22	Sequence 22, Appli	376	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
304	28	3.2	5872	4	US-09-244-794A-23	Sequence 23, Appli	377	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
305	28	3.2	5872	4	US-09-244-794A-24	Sequence 24, Appli	378	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
306	28	3.2	5872	4	US-09-244-794A-25	Sequence 25, Appli	379	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
307	28	3.2	5872	4	US-09-244-794A-26	Sequence 26, Appli	380	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
308	28	3.2	5872	4	US-09-244-794A-27	Sequence 27, Appli	381	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
309	28	3.2	5872	4	US-09-244-794A-28	Sequence 28, Appli	382	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
310	28	3.2	5872	4	US-09-244-794A-29	Sequence 29, Appli	383	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
311	28	3.2	5872	4	US-09-244-794A-30	Sequence 30, Appli	384	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
312	28	3.2	5872	4	US-09-244-794A-31	Sequence 31, Appli	385	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
313	28	3.2	5872	4	US-09-244-794A-32	Sequence 32, Appli	386	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
314	28	3.2	5872	4	US-09-244-794A-33	Sequence 33, Appli	387	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
315	28	3.2	5872	4	US-09-244-794A-34	Sequence 34, Appli	388	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
316	28	3.2	5872	4	US-09-244-794A-35	Sequence 35, Appli	389	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
317	28	3.2	5872	4	US-09-244-794A-36	Sequence 36, Appli	390	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
318	28	3.2	5872	4	US-09-244-794A-37	Sequence 37, Appli	391	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap
319	28	3.2	5872	4	US-09-244-794A-38	Sequence 38, Appli	392	27	3.1	106	4	US-09-621-976-12330	Sequence 1074, Ap

333	27	3.1	170	4	US-09-621-976-19172	Sequence 19172, A	466	27	3.1	282	4	US-09-621-976-18648	Sequence 18648, A
C 334	27	3.1	176	3	US-09-014-416-63	Sequence 63, Appl	467	27	3.1	283	4	US-09-621-976-16989	Sequence 16989, A
C 335	27	3.1	177	4	US-09-621-976-8073	Sequence 8073, Ap	468	27	3.1	289	4	US-09-621-976-15142	Sequence 15142, A
336	27	3.1	179	4	US-09-621-976-18054	Sequence 18054, A	469	27	3.1	291	3	US-09-329-796-1	Sequence 1, Appl1
337	27	3.1	180	4	US-09-621-976-18587	Sequence 18587, A	470	27	3.1	292	4	US-09-621-976-12039	Sequence 12039, A
338	27	3.1	182	4	US-09-621-976-16234	Sequence 16234, A	471	27	3.1	292	4	US-09-621-976-12050	Sequence 12050, A
C 339	27	3.1	183	3	US-09-014-416-60	Sequence 60, Appl	472	27	3.1	293	4	US-09-621-976-12065	Sequence 12065, A
400	27	3.1	184	4	US-09-621-976-13606	Sequence 13606, A	C 473	27	3.1	295	4	US-09-621-976-16965	Sequence 16965, A
401	27	3.1	184	4	US-09-480-921B-13	Sequence 13, Appl	474	27	3.1	297	4	US-09-621-976-1263	Sequence 1263, Ap
402	27	3.1	185	4	US-09-621-976-16538	Sequence 16538, A	475	27	3.1	297	4	US-09-621-976-16032	Sequence 16032, A
403	27	3.1	187	4	US-09-621-976-16539	Sequence 16539, A	C 476	27	3.1	298	2	US-08-520-678A-21	Sequence 21, Appl
404	27	3.1	188	4	US-09-621-976-16542	Sequence 16542, A	C 477	27	3.1	298	2	US-08-897-126-21	Sequence 25, App
405	27	3.1	189	4	US-09-621-976-14761	Sequence 14761, A	C 478	27	3.1	302	4	US-09-439-313-255	Sequence 255, App
406	27	3.1	190	4	US-09-621-976-16540	Sequence 16540, A	C 479	27	3.1	302	4	US-09-332-66A-255	Sequence 255, App
407	27	3.1	191	4	US-09-621-976-9448	Sequence 9448, Ap	C 480	27	3.1	302	4	US-09-232-149A-255	Sequence 255, App
408	27	3.1	191	4	US-09-621-976-16546	Sequence 16546, A	C 481	27	3.1	302	4	US-09-159-812-255	Sequence 255, App
409	27	3.1	193	4	US-09-621-976-10543	Sequence 10543, A	C 482	27	3.1	302	4	US-09-633-215-255	Sequence 255, App
410	27	3.1	193	4	US-09-621-976-16535	Sequence 16535, A	C 483	27	3.1	302	4	US-09-688-166A-255	Sequence 255, App
411	27	3.1	194	4	US-09-621-976-14889	Sequence 14889, A	C 484	27	3.1	302	4	US-09-688-489-255	Sequence 255, App
412	27	3.1	194	4	US-09-621-976-16537	Sequence 16537, A	485	27	3.1	305	4	US-09-621-976-16020	Sequence 16020, A
413	27	3.1	195	4	US-09-621-976-16062	Sequence 16062, A	486	27	3.1	306	4	US-09-621-976-16035	Sequence 16035, A
414	27	3.1	198	4	US-08-330-108-16	Sequence 16, Appl	C 487	27	3.1	321	2	US-08-520-678A-23	Sequence 23, Appl
415	27	3.1	198	5	PCT-US92-10087-16	Sequence 16, Appl	C 488	27	3.1	326	4	US-09-629-645A-17	Sequence 17, Appl
416	27	3.1	199	4	US-09-736-457-102	Sequence 102, App	489	27	3.1	326	4	US-09-621-976-16024	Sequence 16024, A
417	27	3.1	199	4	US-09-736-457-102	Sequence 102, App	490	27	3.1	326	4	US-09-621-976-16012	Sequence 16012, A
418	27	3.1	199	4	US-09-614-124B-102	Sequence 102, App	491	27	3.1	329	4	US-09-621-976-16024	Sequence 16024, A
419	27	3.1	199	4	US-09-671-325-102	Sequence 102, App	492	27	3.1	330	4	US-09-621-976-16031	Sequence 16031, A
420	27	3.1	199	4	US-09-589-184-102	Sequence 102, App	493	27	3.1	332	4	US-09-621-976-16030	Sequence 16030, A
C 421	27	3.1	200	3	US-09-014-416-64	Sequence 64, Appl	494	27	3.1	332	4	US-09-621-976-16050	Sequence 16050, A
422	27	3.1	201	4	US-09-621-976-16551	Sequence 16551, A	495	27	3.1	333	3	US-08-946-026-35	Sequence 35, Appl
423	27	3.1	203	4	US-09-621-976-16454	Sequence 16454, A	C 496	27	3.1	333	4	US-09-621-976-16032	Sequence 16032, A
424	27	3.1	204	4	US-09-621-976-1323	Sequence 1323, Ap	497	27	3.1	333	4	US-09-621-976-16044	Sequence 16044, A
425	27	3.1	209	4	US-09-621-976-12930	Sequence 12930, A	498	27	3.1	334	4	US-09-621-976-16041	Sequence 16041, A
426	27	3.1	213	4	US-09-621-976-16536	Sequence 16536, A	499	27	3.1	336	4	US-09-621-976-16013	Sequence 16013, A
427	27	3.1	217	4	US-09-621-976-16285	Sequence 16285, A	500	27	3.1	336	4	US-09-621-976-16013	Sequence 16013, A
428	27	3.1	221	4	US-09-621-976-13585	Sequence 13585, A	501	27	3.1	337	4	US-09-621-976-16041	Sequence 16041, A
429	27	3.1	222	4	US-09-621-976-16293	Sequence 16293, A	502	27	3.1	338	4	US-09-621-976-16026	Sequence 16026, A
C 430	27	3.1	227	2	US-08-520-678A-28	Sequence 28, Appl	503	27	3.1	347	4	US-09-385-982-283	Sequence 283, App
C 431	27	3.1	227	3	US-08-897-126-28	Sequence 28, Appl	C 504	27	3.1	348	2	US-08-520-678A-22	Sequence 22, Appl
432	27	3.1	228	3	US-09-328-111-484	Sequence 111, App	C 505	27	3.1	356	3	US-08-897-126-22	Sequence 22, Appl
433	27	3.1	231	4	US-09-621-976-16317	Sequence 16317, A	C 506	27	3.1	356	3	US-09-621-976-16581	Sequence 16581, A
434	27	3.1	231	4	US-09-621-976-16536	Sequence 16536, A	507	27	3.1	357	4	US-09-621-976-16058	Sequence 16058, A
435	27	3.1	232	4	US-09-621-976-17701	Sequence 17701, A	508	27	3.1	359	4	US-09-621-976-16010	Sequence 16010, A
436	27	3.1	233	4	US-09-621-976-16559	Sequence 16559, A	509	27	3.1	359	4	US-09-621-976-16010	Sequence 16010, A
437	27	3.1	234	4	US-09-621-976-16557	Sequence 16557, A	510	27	3.1	359	4	US-09-621-976-16019	Sequence 16019, A
438	27	3.1	235	4	US-09-621-976-9455	Sequence 9455, Ap	C 511	27	3.1	362	1	US-08-171-385-12	Sequence 12, Appl
439	27	3.1	235	4	US-09-621-976-16550	Sequence 16550, A	C 512	27	3.1	362	1	US-08-361-441B-12	Sequence 12, Appl
440	27	3.1	240	4	US-09-621-976-1324	Sequence 1324, Ap	513	27	3.1	362	4	US-09-621-976-16010	Sequence 16010, A
441	27	3.1	242	4	US-09-621-976-16340	Sequence 16340, A	514	27	3.1	365	4	US-09-621-976-14693	Sequence 14693, A
442	27	3.1	242	4	US-09-621-976-16340	Sequence 16340, A	515	27	3.1	365	4	US-09-621-976-16042	Sequence 16042, A
443	27	3.1	245	4	US-09-621-976-17945	Sequence 17945, A	516	27	3.1	367	3	US-09-328-111-446	Sequence 446, App
444	27	3.1	246	4	US-09-621-976-16288	Sequence 16288, A	517	27	3.1	371	4	US-09-621-976-16048	Sequence 16048, A
445	27	3.1	247	4	US-09-621-976-17039	Sequence 17039, A	518	27	3.1	375	4	US-09-621-976-18143	Sequence 18143, A
446	27	3.1	248	4	US-09-621-976-9105	Sequence 9105, Ap	C 519	27	3.1	390	4	US-09-222-575-90	Sequence 90, Appl
447	27	3.1	249	4	US-09-621-976-1322	Sequence 1322, Ap	C 520	27	3.1	390	4	US-09-389-681-90	Sequence 90, Appl
448	27	3.1	249	4	US-09-621-976-16291	Sequence 16291, A	C 521	27	3.1	390	4	US-09-620-45B-90	Sequence 90, Appl
449	27	3.1	249	4	US-09-621-976-16292	Sequence 16292, A	C 522	27	3.1	390	4	US-09-339-338-90	Sequence 90, Appl
450	27	3.1	250	4	US-09-621-976-17371	Sequence 17371, A	C 523	27	3.1	390	4	US-09-433-826B-90	Sequence 90, Appl
451	27	3.1	250	4	US-09-621-976-18893	Sequence 18893, A	C 524	27	3.1	390	4	US-09-604-287A-90	Sequence 90, Appl
C 452	27	3.1	253	2	US-08-520-678A-25	Sequence 25, Appl	C 525	27	3.1	390	4	US-09-285-480-90	Sequence 90, Appl
C 453	27	3.1	253	2	US-08-897-126-25	Sequence 25, Appl	C 526	27	3.1	390	4	US-09-621-976-15352	Sequence 15352, A
C 454	27	3.1	257	2	US-08-520-678A-24	Sequence 24, Appl	C 527	27	3.1	390	4	US-09-834-759-90	Sequence 90, Appl
C 455	27	3.1	257	2	US-08-897-126-24	Sequence 24, Appl	C 528	27	3.1	394	4	US-09-621-976-15204	Sequence 15204, A
C 456	27	3.1	259	3	US-08-621-976-16294	Sequence 16294, A	C 529	27	3.1	395	4	US-09-195-106-21	Sequence 21, Appl
C 457	27	3.1	260	3	US-08-520-678A-29	Sequence 29, Appl	C 530	27	3.1	396	4	US-09-640-173-30	Sequence 173, App
C 458	27	3.1	260	3	US-08-897-126-29	Sequence 29, Appl	C 531	27	3.1	396	4	US-09-640-173-131	Sequence 131, App
459	27	3.1	261	4	US-09-621-976-17067	Sequence 17067, A	C 532	27	3.1	396	4	US-09-640-173-140	Sequence 140, App
460	27	3.1	265	4	US-09-621-976-16813	Sequence 16813, A	C 533	27	3.1	396	4	US-09-640-173-165	Sequence 165, App
461	27	3.1	267	2	US-08-924-838-3	Sequence 3, Appl1	C 534	27	3.1	396	4	US-09-713-550-20	Sequence 20, Appl
462	27	3.1	267	2	US-09-621-976-14155	Sequence 14155, A	C 535	27	3.1	396	4	US-09-713-550-131	Sequence 131, App
463	27	3.1	269	4	US-09-621-976-14781	Sequence 14781, A	C 536	27	3.1	396	4	US-09-713-550-140	Sequence 140, App
464	27	3.1	270	4	US-09-621-976-17049	Sequence 17049, A	C 537	27	3.1	396	4	US-09-713-550-165	Sequence 165, App
C 465	27	3.1	271	2	US-08-731-272A-29	Sequence 29, Appl	538	27	3.1	399	4	US-09-621-976-1484	Sequence 1484, App

C 539	-27	3.1	413	3	US-09-328-111-25	Sequence 25, Appl	612	27	3.1	855	6	5223394-3	Patent No. 5223394
C 540	-27	3.1	416	4	US-09-621-976-3320	Sequence 3320, Ap	613	27	3.1	859	3	US-09-347-778-47	Sequence 47, Appl
C 541	-27	3.1	450	4	US-09-385-988-155	Sequence 155, App	614	27	3.1	861	2	US-08-524-759-15	Sequence 15, Appl
C 542	-27	3.1	464	4	US-09-302-769-37	Sequence 37, Appl	615	27	3.1	861	3	US-09-248-335-15	Sequence 15, Appl
C 543	-27	3.1	474	3	US-08-516-859A-97	Sequence 97, Appl	616	27	3.1	863	1	US-07-940-861-11	Sequence 11, Appl
C 544	-27	3.1	474	4	US-09-586-472-97	Sequence 97, Appl	617	27	3.1	863	1	US-08-459-512-11	Sequence 11, Appl
C 545	-27	3.1	474	4	US-09-528-706-97	Sequence 97, Appl	618	27	3.1	863	2	US-08-459-657-11	Sequence 11, Appl
C 546	-27	3.1	495	4	US-09-220-132-186	Sequence 186, App	619	27	3.1	863	2	US-08-460-132-11	Sequence 11, Appl
C 547	-27	3.1	504	4	US-09-796-766-111	Sequence 11, Appl	620	27	3.1	863	5	PCT-US92-02050-11	Sequence 11, Appl
C 548	-27	3.1	520	4	US-09-220-132-111	Sequence 11, App	621	27	3.1	863	6	5185441-35	Patent No. 5185441
C 549	-27	3.1	526	4	US-09-163-748C-2	Sequence 2, Appl1	622	27	3.1	863	6	5223394-5	Patent No. 5223394
C 550	-27	3.1	531	4	US-09-105-542A-12	Sequence 12, Appl	623	27	3.1	872	3	US-09-248-335-63	Sequence 63, Appl
C 551	-27	3.1	538	4	US-09-399-913-37	Sequence 37, Appl	624	27	3.1	873	3	US-09-475-116A-20	Sequence 20, Appl
C 552	-27	3.1	536	1	US-08-341-568-1	Sequence 1, Appl1	625	27	3.1	873	4	US-09-704-640-20	Sequence 20, Appl
C 553	-27	3.1	536	2	US-08-911-020-1	Sequence 1, Appl1	626	27	3.1	874	4	US-09-189-681-426	Sequence 426, App
C 554	-27	3.1	537	4	US-09-720-201A-4	Sequence 4, Appl1	627	27	3.1	874	4	US-09-620-405E-436	Sequence 426, App
C 555	-27	3.1	550	4	US-09-010-147B-5	Sequence 5, Appl1	628	27	3.1	874	4	US-09-433-826E-446	Sequence 426, App
C 556	-27	3.1	564	4	US-09-702-705-1414	Sequence 1414, Ap	629	27	3.1	874	4	US-09-604-887A-426	Sequence 426, App
C 557	-27	3.1	564	4	US-09-736-457-1414	Sequence 1414, Ap	630	27	3.1	874	4	US-09-604-887A-426	Sequence 426, App
C 558	-27	3.1	564	4	US-09-614-124B-1414	Sequence 1414, Ap	631	27	3.1	879	1	US-08-158-682E-1	Sequence 1, Appl1
C 559	-27	3.1	572	3	US-09-671-325-1414	Sequence 644, App	632	27	3.1	879	1	US-08-015-403-1	Sequence 1, Appl1
C 560	-27	3.1	572	3	US-09-328-111-644	Sequence 7, Appl1	633	27	3.1	880	1	US-08-616-368A-7	Sequence 7, Appl1
C 561	-27	3.1	572	3	US-09-357-251-7	Sequence 465, App	634	27	3.1	880	3	US-09-054-298-7	Sequence 7, Appl1
C 562	-27	3.1	578	3	US-09-385-982-465	Sequence 465, App	635	27	3.1	880	3	US-08-818-655-7	Sequence 7, Appl1
C 563	-27	3.1	591	4	US-09-702-705-237	Sequence 237, App	636	27	3.1	882	2	US-09-305-839-7	Sequence 7, Appl1
C 564	-27	3.1	591	4	US-09-736-457-237	Sequence 237, App	637	27	3.1	882	2	US-08-909-965C-9	Sequence 9, Appl1
C 565	-27	3.1	591	4	US-09-614-124B-237	Sequence 237, App	638	27	3.1	888	4	US-09-188-930-13	Sequence 13, Appl
C 566	-27	3.1	591	4	US-09-671-325-237	Sequence 237, App	639	27	3.1	888	4	US-09-312-283C-13	Sequence 13, Appl
C 567	-27	3.1	591	4	US-09-589-184-237	Sequence 237, App	640	27	3.1	890	4	US-09-621-976-2725	Sequence 2725, Ap
C 568	-27	3.1	599	3	US-09-328-111-147	Sequence 147, App	641	27	3.1	906	4	US-09-489-847-72	Sequence 72, Appl
C 569	-27	3.1	603	3	US-09-385-982-251	Sequence 251, App	642	27	3.1	913	3	US-08-651-136C-13	Sequence 13, Appl
C 570	-27	3.1	603	3	US-09-385-982-251	Sequence 251, App	643	27	3.1	913	4	US-09-229-911A-13	Sequence 13, Appl
C 571	-27	3.1	607	3	US-09-328-111-531	Sequence 293, App	644	27	3.1	917	4	US-09-227-357-43	Sequence 43, Appl
C 572	-27	3.1	615	3	US-09-328-111-371	Sequence 371, App	645	27	3.1	940	1	US-08-089-998B-1	Sequence 1, Appl1
C 573	-27	3.1	619	4	US-09-105-542A-2	Sequence 2, Appl1	646	27	3.1	940	5	US-08-457-272-1	Sequence 1, Appl1
C 574	-27	3.1	619	4	US-09-489-847-58	Sequence 58, Appl	647	27	3.1	940	5	PCT-US94-07595-1	Sequence 1, Appl1
C 575	-27	3.1	623	6	5240847-1	Patent No. 5240847	648	27	3.1	944	4	US-09-227-357-122	Sequence 122, App
C 576	-27	3.1	631	4	US-09-328-111-361	Sequence 361, App	649	27	3.1	953	1	US-08-137-793-1	Sequence 1, Appl1
C 577	-27	3.1	644	4	US-09-720-201A-6	Sequence 6, Appl1	650	27	3.1	953	2	US-08-636-176-1	Sequence 1, Appl1
C 578	-27	3.1	656	3	US-09-328-111-587	Sequence 587, App	651	27	3.1	953	5	PCT-US95-01618-1	Sequence 1, Appl1
C 579	-27	3.1	669	3	US-09-328-111-342	Sequence 342, App	652	27	3.1	969	2	US-08-365-486A-27	Sequence 27, Appl
C 580	-27	3.1	674	4	US-09-673-395A-94	Sequence 94, Appl	653	27	3.1	969	3	US-08-880-342-27	Sequence 27, Appl
C 581	-27	3.1	685	4	US-09-489-847-103	Sequence 103, App	654	27	3.1	970	3	US-09-248-335-47	Sequence 47, Appl
C 582	-27	3.1	688	4	US-09-148-545-73	Sequence 73, Appl	655	27	3.1	970	4	US-09-833-381-1294	Sequence 1294, Ap
C 583	-27	3.1	699	4	US-09-690-454-31	Sequence 31, Appl	656	27	3.1	975	4	US-09-381-488-6	Sequence 6, Appl1
C 584	-27	3.1	700	1	US-07-846-992-1	Sequence 1, Appl1	657	27	3.1	997	4	US-09-800-729-14	Sequence 14, Appl
C 585	-27	3.1	700	1	US-08-469-555-1	Sequence 26, Appl1	658	27	3.1	999	4	US-09-699-266A-5	Sequence 5, Appl1
C 586	-27	3.1	700	1	US-09-152-060-26	Sequence 1, Appl1	659	27	3.1	1007	3	US-09-248-335-31	Sequence 31, Appl
C 587	-27	3.1	730	4	US-09-328-475C-283	Sequence 283, App	660	27	3.1	1009	6	5223394-8	Patent No. 5223394
C 588	-27	3.1	737	4	US-09-148-545-127	Sequence 127, App	661	27	3.1	1019	6	US-09-288-143-33	Sequence 33, Appl
C 589	-27	3.1	756	2	US-08-530-165-1	Sequence 1, Appl1	662	27	3.1	1023	3	US-08-554-385-4	Sequence 4, Appl1
C 590	-27	3.1	775	3	US-09-361-434-6	Sequence 6, Appl1	663	27	3.1	1032	4	US-09-257-179-21	Sequence 21, Appl
C 591	-27	3.1	775	3	US-09-361-434-8	Sequence 8, Appl1	664	27	3.1	1039	4	US-09-464-535-23	Sequence 23, Appl
C 592	-27	3.1	775	4	US-09-635-025-6	Sequence 6, Appl1	665	27	3.1	1047	1	US-08-403-378B-3	Sequence 3, Appl1
C 593	-27	3.1	775	4	US-09-635-025-8	Sequence 8, Appl1	666	27	3.1	1052	4	US-09-592-891A-8	Sequence 8, Appl1
C 594	-27	3.1	776	4	US-09-902-331B-3	Sequence 3, Appl1	667	27	3.1	1057	4	US-09-716-129-16	Sequence 16, Appl
C 595	-27	3.1	776	4	US-09-205-258-201	Sequence 20, App	668	27	3.1	1071	4	US-09-800-729-45	Sequence 45, Appl
C 596	-27	3.1	782	4	US-09-621-976-1700	Sequence 1700, Ap	669	27	3.1	1078	6	5223394-10	Patent No. 5223394
C 597	-27	3.1	810	3	US-09-363-970-4	Sequence 4, Appl1	670	27	3.1	1086	4	US-09-800-729-48	Sequence 48, Appl
C 598	-27	3.1	833	4	US-09-308-386A-2	Sequence 2, Appl1	671	27	3.1	1097	4	US-09-461-325-84	Sequence 84, Appl
C 599	-27	3.1	832	4	US-09-280-839-1	Sequence 1, Appl1	672	27	3.1	1097	4	US-10-012-542-84	Sequence 84, Appl
C 600	-27	3.1	832	4	US-09-152-060-27	Sequence 27, Appl	673	27	3.1	1100	4	US-09-372-422A-47	Sequence 47, Appl
C 601	-27	3.1	836	2	US-08-698-805-7	Sequence 7, Appl1	674	27	3.1	1106	3	US-09-361-434-16	Sequence 16, Appl
C 602	-27	3.1	841	3	US-09-004-731-40	Sequence 40, Appl	675	27	3.1	1106	3	US-09-361-434-18	Sequence 18, Appl
C 603	-27	3.1	841	3	US-09-004-731-42	Sequence 42, Appl	676	27	3.1	1106	4	US-09-635-025-16	Sequence 16, Appl
C 604	-27	3.1	841	3	US-09-032-215-46	Sequence 46, Appl	677	27	3.1	1106	4	US-09-635-025-16	Sequence 16, Appl
C 605	-27	3.1	841	3	US-09-032-215-48	Sequence 48, Appl	678	27	3.1	1113	2	US-08-907-492A-13	Sequence 13, Appl1
C 606	-27	3.1	841	3	US-08-749-699-40	Sequence 40, Appl	679	27	3.1	1115	3	US-08-190-802A-19	Sequence 19, Appl
C 607	-27	3.1	841	3	US-08-749-699-42	Sequence 42, Appl	680	27	3.1	1115	3	US-08-477-346-19	Sequence 19, Appl
C 608	-27	3.1	841	4	US-09-004-729-40	Sequence 40, Appl	681	27	3.1	1115	4	US-08-473-089-19	Sequence 19, Appl
C 609	-27	3.1	847	4	US-09-004-729-42	Sequence 42, Appl	682	27	3.1	1117	4	US-08-487-072A-19	Sequence 19, Appl
C 610	-27	3.1	847	4	US-09-149-476-205	Sequence 205, App	683	27	3.1	1117	4	US-09-148-545-54	Sequence 54, Appl
C 611	-27	3.1	855	6	5185441-40	Patent No. 5185441	684	27	3.1	1124	4	US-09-386-149-11	Sequence 11, Appl

685	27	3.1	1127	4	US-09-391-741A-1	Sequence 1, Appl	758	27	3.1	1397	4	US-09-216-393B-345	Sequence 345, App
686	27	3.1	1127	4	US-09-391-741A-15	Sequence 15, Appl	759	27	3.1	1504	4	US-09-205-258-223	Sequence 223, App
687	27	3.1	1127	4	US-09-391-741A-25	Sequence 25, Appl	760	27	3.1	1408	4	US-08-254-404-21	Sequence 21, Appl
688	27	3.1	1133	3	US-08-983-409-5	Sequence 5, Appl	761	27	3.1	1408	2	US-08-327-451E-71	Sequence 21, Appl
689	27	3.1	1133	4	US-09-483-273-95	Sequence 95, Appl	762	27	3.1	1408	2	US-08-458-109-21	Sequence 27, Appl
690	27	3.1	1138	4	US-09-800-729-44	Sequence 44, Appl	763	27	3.1	1447	2	US-09-443-041A-27	Sequence 27, Appl
691	27	3.1	1143	4	US-09-220-132-166	Sequence 166, App	764	27	3.1	1454	2	US-08-713-000-7	Sequence 7, Appl
692	27	3.1	1147	1	US-08-668-716-1	Sequence 1, Appl	765	27	3.1	1454	2	US-08-975-316-7	Sequence 7, Appl
693	27	3.1	1149	4	US-09-800-729-47	Sequence 47, Appl	766	27	3.1	1454	4	US-09-211-710-7	Sequence 7, Appl
694	27	3.1	1153	4	US-09-372-448A-5	Sequence 5, Appl	767	27	3.1	1454	4	US-09-615-192A-7	Sequence 7, Appl
695	27	3.1	1153	4	US-09-149-476-41	Sequence 41, Appl	768	27	3.1	1454	4	US-09-169-789-7	Sequence 7, Appl
696	27	3.1	1172	4	US-09-461-325-106	Sequence 106, App	769	27	3.1	1460	4	US-09-615-192A-35	Sequence 95, Appl
697	27	3.1	1172	4	US-10-012-542-106	Sequence 106, App	770	27	3.1	1460	4	US-09-169-789-95	Sequence 95, Appl
698	27	3.1	1175	4	US-09-461-325-15	Sequence 15, Appl	771	27	3.1	1474	2	US-08-975-316-71	Sequence 71, Appl
699	27	3.1	1175	4	US-10-012-542-15	Sequence 15, Appl	772	27	3.1	1474	4	US-09-615-192A-71	Sequence 71, Appl
700	27	3.1	1179	4	US-09-149-476-67	Sequence 67, App	773	27	3.1	1474	4	US-09-615-192A-702	Sequence 402, App
701	27	3.1	1181	3	US-09-328-796-2	Sequence 2, Appl	774	27	3.1	1474	4	US-09-328-932A-102	Sequence 202, App
702	27	3.1	1192	4	US-09-439-554-23	Sequence 23, Appl	775	27	3.1	1474	4	US-09-169-789-71	Sequence 71, Appl
703	27	3.1	1193	4	US-09-372-442A-23	Sequence 23, Appl	776	27	3.1	1474	4	US-09-169-789-184	Sequence 184, App
704	27	3.1	1208	4	US-09-205-258-25	Sequence 25, Appl	777	27	3.1	1477	4	US-09-585-173B-7	Sequence 7, Appl
705	27	3.1	1215	1	US-08-593-214A-1	Sequence 1, Appl	778	27	3.1	1493	5	5340934-5	Parent No. 5340934
706	27	3.1	1215	3	US-09-148-976-1	Sequence 1, Appl	779	27	3.1	1500	5	PCT-US93-08386-3	Sequence 3, Appl
707	27	3.1	1215	4	US-09-220-132-184	Sequence 184, App	780	27	3.1	1503	4	US-09-907-794A-220	Sequence 220, App
708	27	3.1	1216	4	US-09-533-029-121	Sequence 121, App	781	27	3.1	1503	4	US-09-905-125A-220	Sequence 220, App
709	27	3.1	1217	3	US-09-225-244-1	Sequence 1, Appl	782	27	3.1	1503	4	US-09-902-775A-220	Sequence 220, App
710	27	3.1	1217	3	US-09-417-242-1	Sequence 1, Appl	783	27	3.1	1511	2	US-08-809-763-3	Sequence 3, Appl
711	27	3.1	1227	2	US-08-903-851-1	Sequence 1, Appl	784	27	3.1	1511	2	US-08-956-253-3	Sequence 3, Appl
712	27	3.1	1236	1	US-09-694-094-2	Sequence 2, Appl	785	27	3.1	1513	4	US-09-301-666A-9	Sequence 9, Appl
713	27	3.1	1240	1	US-08-388-756-1	Sequence 1, Appl	786	27	3.1	1513	4	US-09-301-217-9	Sequence 9, Appl
714	27	3.1	1240	2	US-08-746-428-1	Sequence 1, Appl	787	27	3.1	1527	4	US-09-244-111-7	Sequence 7, Appl
715	27	3.1	1243	1	US-08-178-606-1	Sequence 1, Appl	788	27	3.1	1536	4	US-09-082-358B-1	Sequence 1, Appl
716	27	3.1	1263	1	US-08-314-309A-24	Sequence 24, Appl	789	27	3.1	1537	2	US-08-839-008-1	Sequence 1, Appl
717	27	3.1	1267	1	US-08-140-797-1	Sequence 1, Appl	790	27	3.1	1541	4	US-09-149-476-65	Sequence 65, Appl
718	27	3.1	1267	4	US-08-466-670A-1	Sequence 1, Appl	791	27	3.1	1544	4	US-09-187-999-14	Sequence 14, Appl
719	27	3.1	1276	3	US-09-716-129-40	Sequence 40, Appl	792	27	3.1	1558	1	US-08-467-607-2	Sequence 2, Appl
720	27	3.1	1279	3	US-09-248-335-25	Sequence 25, Appl	793	27	3.1	1558	2	US-08-468-362-2	Sequence 2, Appl
721	27	3.1	1280	4	US-09-369-247-40	Sequence 40, Appl	794	27	3.1	1558	2	US-08-850-332-2	Sequence 2, Appl
722	27	3.1	1293	1	US-08-317-522A-6	Sequence 6, Appl	795	27	3.1	1559	2	US-08-417-174-1	Sequence 1, Appl
723	27	3.1	1293	2	US-08-753-818A-6	Sequence 6, Appl	796	27	3.1	1559	2	US-08-231-565A-1	Sequence 1, Appl
724	27	3.1	1293	2	US-08-751-965-6	Sequence 6, Appl	797	27	3.1	1559	2	US-09-007-961-1	Sequence 1, Appl
725	27	3.1	1293	2	US-08-738-975-6	Sequence 6, Appl	798	27	3.1	1559	3	US-09-267-439-1	Sequence 1, Appl
726	27	3.1	1293	2	US-08-728-626-6	Sequence 6, Appl	799	27	3.1	1559	4	US-09-073-138-1	Sequence 1, Appl
727	27	3.1	1293	2	US-08-808-559A-6	Sequence 6, Appl	800	27	3.1	1562	1	US-08-330-108-1	Sequence 1, Appl
728	27	3.1	1296	1	US-08-385-151A-1	Sequence 1, Appl	801	27	3.1	1562	5	PCT-US92-10087-1	Sequence 1, Appl
729	27	3.1	1296	4	US-08-472-402A-1	Sequence 1, Appl	802	27	3.1	1573	4	US-09-216-393B-292	Sequence 292, App
730	27	3.1	1298	1	US-08-361-708-1	Sequence 1, Appl	803	27	3.1	1573	4	US-09-216-393B-294	Sequence 294, App
731	27	3.1	1298	1	US-08-536-277-1	Sequence 1, Appl	804	27	3.1	1584	1	US-08-483-432-24	Sequence 24, Appl
732	27	3.1	1300	4	US-09-419-679-7	Sequence 7, Appl	805	27	3.1	1584	1	US-08-483-432-24	Sequence 24, Appl
733	27	3.1	1302	4	US-09-323-409-91	Sequence 91, Appl	806	27	3.1	1584	1	US-08-745-995A-1	Sequence 1, Appl
734	27	3.1	1302	4	US-09-323-409-93	Sequence 93, Appl	807	27	3.1	1584	1	US-08-745-995A-3	Sequence 3, Appl
735	27	3.1	1302	4	US-09-451-537-91	Sequence 91, Appl	808	27	3.1	1584	4	US-09-005-352-3	Sequence 3, Appl
736	27	3.1	1302	4	US-09-451-537-93	Sequence 93, Appl	809	27	3.1	1584	4	US-09-005-352-3	Sequence 3, Appl
737	27	3.1	1315	3	US-09-164-193-1	Sequence 1, Appl	810	27	3.1	1584	4	US-09-724-864-5	Sequence 5, Appl
738	27	3.1	1315	3	US-09-164-193-1	Sequence 1, Appl	811	27	3.1	1587	4	US-09-724-864-5	Sequence 5, Appl
739	27	3.1	1325	1	US-08-306-691B-51	Sequence 51, Appl	812	27	3.1	1595	4	US-09-738-946-13	Sequence 13, Appl
740	27	3.1	1325	2	US-08-464-517-1	Sequence 1, Appl	813	27	3.1	1606	4	US-09-820-004-1	Sequence 1, Appl
741	27	3.1	1325	2	US-08-246-351A-1	Sequence 1, Appl	814	27	3.1	1619	4	US-09-522-714-11	Sequence 11, Appl
742	27	3.1	1325	3	US-08-463-772-1	Sequence 1, Appl	815	27	3.1	1630	4	US-10-162-012-39	Sequence 39, Appl
743	27	3.1	1325	3	US-09-412-102-3	Sequence 3, Appl	816	27	3.1	1652	4	US-09-627-650B-2	Sequence 2, Appl
744	27	3.1	1325	3	US-09-217-787-3	Sequence 3, Appl	817	27	3.1	1652	4	US-09-436-063C-2	Sequence 2, Appl
745	27	3.1	1325	5	PCT-US93-05000-1	Sequence 1, Appl	818	27	3.1	1654	4	US-08-991-426-3	Sequence 3, Appl
746	27	3.1	1335	4	US-09-482-273-80	Sequence 80, Appl	819	27	3.1	1654	3	US-09-147-470-3	Sequence 3, Appl
747	27	3.1	1342	4	US-09-500-569-9	Sequence 9, Appl	820	27	3.1	1654	4	US-08-648-006A-3	Sequence 3, Appl
748	27	3.1	1342	4	US-09-971-823B-9	Sequence 9, Appl	821	27	3.1	1654	4	US-09-771-023-3	Sequence 3, Appl
749	27	3.1	1354	4	US-09-097-319A-5	Sequence 5, Appl	822	27	3.1	1687	1	US-08-143-219-26	Sequence 26, Appl
750	27	3.1	1354	4	US-09-614-912-37	Sequence 37, Appl	823	27	3.1	1688	2	US-08-433-814-2	Sequence 2, Appl
751	27	3.1	1375	4	US-09-372-422A-37	Sequence 37, Appl	824	27	3.1	1699	4	US-09-153-060-19	Sequence 19, Appl
752	27	3.1	1377	3	US-09-461-474-5	Sequence 5, Appl	825	27	3.1	1700	4	US-09-833-381-1885	Sequence 1885, App
753	27	3.1	1378	4	US-09-149-476-208	Sequence 208, App	826	27	3.1	1703	2	US-08-794-795-1	Sequence 1, Appl
754	27	3.1	1384	4	US-09-227-357-142	Sequence 142, App	827	27	3.1	1703	4	US-09-248-200-1	Sequence 1, Appl
755	27	3.1	1393	1	US-08-174-467-182	Sequence 18, Appl	828	27	3.1	1713	4	US-09-000-062-1	Sequence 1, Appl
756	27	3.1	1393	3	US-08-452-071-18	Sequence 18, Appl	829	27	3.1	1713	4	US-08-945-144A-1	Sequence 1, Appl
757	27	3.1	1397	4	US-09-216-393B-343	Sequence 343, App	830	27	3.1	1716	2	US-08-954-333-9	Sequence 9, Appl

[illegible]

977 27 3.1 2431 1 US-08-456-201-25 Sequence 25, Appl
978 27 3.1 2431 2 US-08-456-241-25 Sequence 25, Appl
979 27 3.1 2431 5 PCT-US92-04295A-25 Sequence 25, Appl
980 27 3.1 2444 3 US-08-906-791-1 Sequence 1, Appl
981 27 3.1 2454 3 US-08-890-615-1 Sequence 1, Appl
982 27 3.1 2454 4 US-09-246-290A-1 Sequence 1, Appl
983 27 3.1 2469 3 US-09-111-730-5 Sequence 5, Appl
984 27 3.1 2469 4 US-09-848-334-1 Sequence 1, Appl
985 27 3.1 2469 4 US-10-274-878-1 Sequence 1, Appl
986 27 3.1 2481 2 US-08-630-118A-1 Sequence 1, Appl
987 27 3.1 2481 2 US-08-838-399-1 Sequence 1, Appl
988 27 3.1 2481 3 US-09-235-839-1 Sequence 1, Appl
989 27 3.1 2481 4 US-09-327-035-1 Sequence 1, Appl
990 27 3.1 2485 4 US-09-889-463A-9 Sequence 9, Appl
991 27 3.1 2524 1 US-08-317-522A-1 Sequence 1, Appl
992 27 3.1 2524 1 US-08-433-818A-1 Sequence 1, Appl
993 27 3.1 2524 2 US-08-751-965-1 Sequence 1, Appl
994 27 3.1 2524 2 US-08-738-975-1 Sequence 1, Appl
995 27 3.1 2524 2 US-08-728-626-1 Sequence 1, Appl
996 27 3.1 2524 3 US-08-808-599A-1 Sequence 1, Appl
997 27 3.1 2535 4 US-09-672-749-10 Sequence 10, Appl
998 27 3.1 2550 1 US-08-245-295-10 Sequence 10, Appl
999 27 3.1 2550 1 US-08-481-130-10 Sequence 10, Appl
1000 27 3.1 2550 1 US-08-656-984A-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-448-606-5
Sequence 5, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmeren, Erik
APPLICANT: Kalden n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 117..847
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 54..116
FEATURE:
NAME/KEY: CDS
LOCATION: 54..847
US-08-448-606-5
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-336-643A-29
Sequence 29, Application US/09336643A
Patent No. 639761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 639761e1 Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1998-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 1111
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)...(957)
OTHER INFORMATION: K-Hnov44, splice 2
US-09-336-643A-29
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1  APPLICANT: Curran, Mark Edward
2  APPLICANT: Hu, Ping
3  APPLICANT: Rutter, Marc
4  APPLICANT: Wang, Jian-Wang
5  TITLE OF INVENTION: No. 6399761el Human Po
6  FILE REFERENCE: SEQ-15P
7  CURRENT APPLICATION NUMBER: US/09/336,643A
8  CURRENT FILING DATE: 1999-06-18
9  PRIOR APPLICATION NUMBER: 60/076,587
10 PRIOR FILING DATE: 1998-08-07
11 PRIOR APPLICATION NUMBER: 60/116,448
12 PRIOR FILING DATE: 1999-01-19
13 PRIOR APPLICATION NUMBER: PCT/US99/03826
14 NUMBER OF SEQ. ID NOS: 87
15 SOFTWARE: PastedSeq for Windows Version 4.0
16 SEQ ID NO 28
17 LENGTH: 1246
18 TYPE: DNA
19 ORGANISM: H. sapiens
20 FEATURE:
21 NAME/KEY: CDS
22 LOCATION: (43)..(1092)
23 OTHER INFORMATION: K+Hnov44, splice 1
24 US-09-336-643A-28

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Query Match      3.6%; Score 31; DB 4; Length 1246;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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RESULT 4
US-09-621-976-16516
; Sequence 16516, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCES: GENSET, 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.fm
; SEQ ID NO 16516
; LENGTH: 157
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-16516

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Query Match	3.5%	Score 30	DB 4	length 197
Best Local Similarity	100.0%	Pred. No. 0.0014		
Matches	30	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	839	TCGGCAAAAAAAAAAAAAAAAAAAAA	868	
Db	165	TCGGCAAAAAAAAAAAAAAAAAAAAA	194	

RESULT 5
US-09-621-976-16515
Sequence 16515 Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Coderre, S.
TITLE OF INVENTION: Ests and Encoded Human Proteins

```

; FILE REFERENCE: GENSEP.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16515
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16515

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Query Match 3.5%; Score 30; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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US-09-621-976-2738
US-09-621-976-2738
Sequence 2738, Application US/09621976
Patent No. 6639053
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ubbett, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2738
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 13..162
US-09-621-976-2738

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Query Match 3.5%; Score 30; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	839	TTGGAAAAAAAAAAAAAAAAAAAAAAAA	868
DB	410	TGGGAAAAAAAAAAAAAAAAAAAAAAAA	439

RESULT 7
 US-09-342-653-5
 Sequence 5, Application US/09342653
 Patent No. 6306632
 GENERAL INFORMATION:
 APPLICANT: Canon, Rebecca E.
 TITLE OF INVENTION: Chromatin Associated Proteins
 FILE REFERENCE: BB-1118
 CURRENT APPLICATION NUMBER: US/09/342,653
 CURRENT FILING DATE: 1999-06-29
 EARLIER APPLICATION NUMBER: 60/092,841
 EARLIER FILING DATE: July 14, 1998
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 5
 LENGTH: 572
 TYPE: DNA
 ORGANISM: Triticum aestivum
 US-09-342-653-5

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; EARLIER FILING DATE: July 14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 9
; SEQ ID NO 5
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Trilicium aestivum
US-09-342-653-5

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Query Match 3.5%; Score 30; DB 4; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAA 868
DB 470 TGGGAAAAAAAAAAAAAAAAAAAAA 499

RESULT 8
US-08-225-757B-1
Sequence 1, Application US/08225757B
Patent No. 5506133
GENERAL INFORMATION:
APPLICANT: YU, ET AL.
TITLE OF INVENTION: Superoxide Dismutase-4
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,757B
FILING DATE: 11 APR-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-225-757B-1

Query Match 3.5%; Score 30; DB 1; Length 1080;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAA 868
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAAA 1071

RESULT 9
US-08-722-050-1
Sequence 1, Application US/08722050
Patent No. 5871729
GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
APPLICANT: FRASER, CLAIRE M.
APPLICANT: COCAVNE, JEANNINE D.
TITLE OF INVENTION: SUPEROXIDE DISMUTASE-4
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,050
FILING DATE: 23-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,757
FILING DATE: 11-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFF, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1020001/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (CDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 115..879
US-08-722-050-1

Query Match 3.5%; Score 30; DB 2; Length 1080;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAA 868
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAAA 1071

RESULT 10
US-09-883-985-1
Sequence 1, Application US/09883985
Patent No. 6635252
GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
APPLICANT: FRASER, CLAIRE M.
APPLICANT: COCAVNE, JEANNINE D.
TITLE OF INVENTION: SUPEROXIDE DISMUTASE-4
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,985
FILING DATE: 20-Jan-2001


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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 09/203,607
  FILING DATE: 02-DEC-1998
  APPLICATION NUMBER: US 08/722,050
  FILING DATE: 23-JAN-1997
  APPLICATION NUMBER: US 08/225,757
  FILING DATE: 11-APR-1994
ATTORNEY/AGENT INFORMATION:
  NAME: STEFFE, ERIC K.
  REGISTRATION NUMBER: 36,688
  REFERENCE/DOCKET NUMBER: 1488.1020003
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1080 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (CDNA)
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 115..879
    SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-883-985-1

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAA 1071

RESULT 11
US-09-501-115-19
; Sequence 19, Application US/09501115
; Patent No. 6552249
; GENERAL INFORMATION:
; APPLICANT: Canoon, Rebecca E.
; APPLICANT: Fader, Gary M.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
; FILE REFERENCE: B01328 US NA
; CURRENT APPLICATION NUMBER: US/09/501,115
; EARLIER FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,585
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1310
; TYPE: DNA
; ORGANISM: Glycine max
US-09-501-115-19

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1272 TGGGAAAAAAAAAAAAAAAAAAAA 1301

RESULT 12
US-08-964-127-5
; Sequence 5, Application US/08964127
; Patent No. 6277565
; GENERAL INFORMATION:

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APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
  ADDRESS: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  OPERATING SYSTEM: Windows 95
  SOFTWARE: FASTSEQ for Windows Version 2.0b
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE: 06-NOV-1997
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE: 06-NOV-1997
      REFERENCE/DOCKET NUMBER: 07334/038001
      TELEPHONE: 617/542-5070
      TELEFAX: 617/542-8906
      TELEX: 200154
    INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1411 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      FEATURE:
        NAME/KEY: Coding Sequence
        LOCATION: 1...966
US-08-964-127-5

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1309 TGGGAAAAAAAAAAAAAAAAAAAA 1338

RESULT 13
US-09-496-692-5
; Sequence 5, Application US/09496692
; Patent No. 6313271
; GENERAL INFORMATION:
; APPLICANT: Grandearl, Andrew David John
; TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
  ADDRESS: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  OPERATING SYSTEM: Windows 95
  SOFTWARE: FASTSEQ for Windows Version 2.0b
  CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/496,692
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,127
FILING DATE: 06-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...966
US-09-496-692-5

Query Match 3.5%; Score 30; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1309 TGGGAAAAAAAAAAAAAAAAAAAA 1338

RESULT 14
US-10-000-273-5
Sequence 5, Application US/10000273
Patent No. 6573057
GENERAL INFORMATION:
APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,273
FILING DATE: 02-NOV-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...966
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-000-273-5

Query Match 3.5%; Score 30; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1309 TGGGAAAAAAAAAAAAAAAAAAAA 1338

RESULT 15
US-09-404-296B-9
Sequence 9, Application US/09404296B
Patent No. 6559358
GENERAL INFORMATION:
APPLICANT: MURRAY, James Augustus Henry
TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
FILE REFERENCE: 2121-0151P
CURRENT APPLICATION NUMBER: US/09/404,296B
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1414
TYPE: DNA
ORGANISM: Helianthus tuberosus
FEATURE:
NAME/KEY: CDS
LOCATION: (48)..(1118)
OTHER INFORMATION: cDNA encoding CYCD3;1
US-09-404-296B-9

Query Match 3.5%; Score 30; DB 4; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868
DB 1371 TGGGAAAAAAAAAAAAAAAAAAAA 1400

Search completed: September 26, 2004, 02:46:57
Job time : 93.0087 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 20:24:57; Search time 403.034 Seconds
(without alignments)
9149.204 Million cell updates/sec

Title: US-10-069-527-1

Perfect score: 868
Sequence: 1 atgggagcgtgggaagcttga.....aaaaaaaaaaaaaaaaaaaa 868

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 3373863 seqs, 2124059041 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	70	8.1	121 6 ABK25454	ABK25454 Male-ster
3	70	8.1	121 6 ABK25462	ABK25462 Male-ster
4	70	8.1	121 6 ABK25466	ABK25466 Male-ster
5	70	8.1	121 6 ABK25458	ABK25458 Male-ster
6	70	8.1	121 6 ABK25453	ABK25453 Male-ster
7	70	8.1	121 6 ABK25465	ABK25465 Male-ster
8	70	8.1	121 6 ABK25461	ABK25461 Male-ster
9	70	8.1	121 6 ABK25457	ABK25457 Male-ster
10	34	3.9	1964 2 AAX27168	AAX27168 Rat GMB-1
11	34	3.9	1330 8 ADA02946	ADA02946 Mouse Nek
12	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
13	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
14	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
15	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
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20	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
21	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
22	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek
23	34	3.9	3130 9 ADB72684	ADB72684 Mouse Nek

97	31	3.6	2714	10	ADD74476	ADD74476 Human PRO	170	30	3.5	906	7	ABX11543	Abx11543 cDNA enco
98	31	3.6	2714	10	ADD77004	ADD77004 Novel hum	171	30	3.5	980	2	AA373471	Aa373471 Human sec
99	31	3.6	2714	10	ADD85698	ADD85698 Novel hum	172	30	3.5	1066	7	ABX11288	Abx11288 Human CDN
100	31	3.6	2714	10	ADE05247	Ade05247 Human PRO	173	30	3.5	1066	7	ABX16282	Abx16282 Human CDN
101	31	3.6	2714	10	ADD74722	ADD74722 Human PRO	174	30	3.5	1066	7	ADCO6719	Adc06719 Human TW4
102	31	3.6	2981	4	ABK43893	Abk43893 DNA enco	175	30	3.5	1080	2	AAT04682	Aat04682 Human sup
103	31	3.6	3840	3	AA600046	AA600046 Human sec	176	30	3.5	1132	2	AAC99108	Aac99108 Human pan
104	30	3.5	46	6	ABK30184	Abk30184 CYP2D6 ge	177	30	3.5	1166	3	AAC98204	Aac98204 Human col
105	30	3.5	68	5	ABV34579	Abv34579 Human pro	178	30	3.5	1199	9	ADDA6756	Add6756 Human gen
106	30	3.5	68	5	ABV43435	Abv43435 Human pro	179	30	3.5	1199	9	ADBS5553	Adbs5553 Human gen
107	30	3.5	79	6	ABQ95007	Abq95007 Tumour su	180	30	3.5	1232	2	AAV40526	Aav40526 Homo sagl
108	30	3.5	139	6	AA24170	AA24170 Human bre	181	30	3.5	1310	8	ADA38394	Ada38394 Soybean c
109	30	3.5	141	6	ABL81058	Ab181058 Human ova	182	30	3.5	1312	9	ADD44858	Add44858 Rat gene
110	30	3.5	160	6	ABQ94748	Abq94748 Tumour su	183	30	3.5	1327	6	ABK54134	Abk54134 cDNA enco
111	30	3.5	165	5	ABV61544	Abv61544 Human pro	184	30	3.5	1349	3	AACT77734	Aact77734 Human can
112	30	3.5	166	6	ABQ94997	Abq94997 Tumour su	185	30	3.5	1351	4	AA262200	Aa262200 Human CDN
113	30	3.5	169	6	ABQ95000	Abq95000 Tumour su	186	30	3.5	1351	7	ABX73541	Abx73541 Human tov
114	30	3.5	198	5	ABV61836	Abv61836 Human pro	187	30	3.5	1351	7	ABBS5701	Abbs5701 Mouse CDN
115	30	3.5	217	4	AA807780	AA807780 Cervical	188	30	3.5	1356	7	AAA64190	Aaa64190 Nucleotid
116	30	3.5	222	5	ABV56932	Abv56932 Human pro	189	30	3.5	1400	3	AAH34413	Aah34413 Human col
117	30	3.5	234	4	AA115324	AA115324 Human bre	190	30	3.5	1411	2	AAH38673	Aah38673 Rat organ
118	30	3.5	245	4	AA125924	AA125924 Human pro	191	30	3.5	1414	2	AAV33888	Aav33888 H.tuberos
119	30	3.5	268	5	ABV57845	Abv57845 Human pro	192	30	3.5	1534	4	AA841556	Aa841556 cDNA enco
120	30	3.5	284	5	ABV57877	Abv57877 Human pro	193	30	3.5	1534	4	AA835046	Aa835046 cDNA enco
121	30	3.5	294	5	AAQ98609	AAQ98609 Human col	194	30	3.5	1534	4	ADC46204	Adc46204 Human tco
122	30	3.5	294	5	ABV61758	Abv61758 Human pro	195	30	3.5	1534	9	AA826079	Aa826079 Human CDN
123	30	3.5	304	5	ABV07230	Abv07230 Human pro	196	30	3.5	1613	4	ABX73420	Abx73420 Human nov
124	30	3.5	352	5	ABV46492	Abv46492 Human pro	197	30	3.5	1613	7	AA862515	Aa862515 cDNA spec
125	30	3.5	363	4	AA180642	AA180642 Human pol	198	30	3.5	1690	6	ABX91984	Abx91984 Lung spec
126	30	3.5	367	4	AA187525	AA187525 Human pol	199	30	3.5	1794	3	AACT6186	Aact6186 Human ORF
127	30	3.5	377	5	ABV61233	Abv61233 Human pro	200	30	3.5	1853	6	AA897011	Aa897011 DNA enco
128	30	3.5	382	4	AA183142	AA183142 Human pol	201	30	3.5	1861	6	AA804194	Aa804194 Human mRN
129	30	3.5	384	4	AA191176	AA191176 Human pol	202	30	3.5	1891	4	AA802543	Aa802543 Human sec
130	30	3.5	407	4	AA186392	AA186392 Human pol	203	30	3.5	1928	6	ABK69104	Abk69104 DNA enco
131	30	3.5	405	4	AA192234	AA192234 Human pol	204	30	3.5	2013	4	AAH34803	Aah34803 Human col
132	30	3.5	406	4	AA191277	AA191277 Human pol	205	30	3.5	2015	2	AA224904	Aa224904 Human sec
133	30	3.5	406	6	ABK64145	Abk64145 Human ben	206	30	3.5	2132	6	ABE50334	AbE50334 Human can
134	30	3.5	406	8	ACH21552	ACH21552 Human adu	207	30	3.5	2265	4	AA846228	Aa846228 Human DNA
135	30	3.5	408	8	ACH35167	ACH35167 Human end	208	30	3.5	2265	6	ABL88243	Ab188243 Human PRO
136	30	3.5	414	4	AA186277	AA186277 Human pol	209	30	3.5	2265	6	ABL95732	Ab195732 Human ang
137	30	3.5	415	3	AAAC59163	AAAC59163 Human sec	210	30	3.5	2265	7	ABX78831	Abx78831 Human PRO
138	30	3.5	416	5	ABV60942	ABV60942 Human pro	211	30	3.5	2265	7	ACA75803	AcA75803 Novel hum
139	30	3.5	419	4	AA188389	AA188389 Human pol	212	30	3.5	2265	7	ACA71283	AcA71283 Human sec
140	30	3.5	423	2	AAK25073	AAK25073 Tobacco N	213	30	3.5	2265	7	ACC87811	Acc87811 Human sec
141	30	3.5	425	8	ACH18956	ACH18956 Human adu	214	30	3.5	2265	7	ACC87197	Acc87197 Human sec
142	30	3.5	428	6	ABK34292	ABK34292 Human CDN	215	30	3.5	2265	7	ACD04370	AcD04370 Human sec
143	30	3.5	432	8	ACH27134	ACH27134 Human adu	216	30	3.5	2265	7	ACA90546	AcA90546 Novel hum
144	30	3.5	433	8	ACH17038	ACH17038 Human pol	217	30	3.5	2265	7	ACC89653	Acc89653 Human sec
145	30	3.5	437	4	AA193105	AA193105 Human pol	218	30	3.5	2265	7	ACA98444	AcA98444 Novel hum
146	30	3.5	459	8	ACH40535	ACH40535 Human foe	219	30	3.5	2265	7	ACH94086	ACH94086 Human sec
147	30	3.5	472	8	ACH34420	ACH34420 Human end	220	30	3.5	2265	7	ACD15479	AcD15479 Human sec
148	30	3.5	481	4	AA119882	AA119882 Human bre	221	30	3.5	2265	7	ACD09066	AcD09066 Human sec
149	30	3.5	483	4	AA182236	AA182236 Human pol	222	30	3.5	2265	7	ACC96986	Acc96986 Human sec
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151	30	3.5	491	8	ACH35435	ACH35435 Human bre	224	30	3.5	2265	7	ACA73074	AcA73074 Human PRO
152	30	3.5	499	4	AA119089	AA119089 Human bre	225	30	3.5	2265	7	ACD03246	AcD03246 Novel hum
153	30	3.5	503	5	ABV60802	ABV60802 Human pro	226	30	3.5	2265	7	ACD02061	AcD02061 Novel hum
154	30	3.5	520	6	ABN61470	ABN61470 Human can	227	30	3.5	2265	7	ACA92253	AcA92253 Novel hum
155	30	3.5	521	5	ABV60685	ABV60685 Human pro	228	30	3.5	2265	7	ACA89678	AcA89678 cDNA enco
156	30	3.5	536	5	ABV61310	ABV61310 Human pro	229	30	3.5	2265	7	ACA73688	AcA73688 Human sec
157	30	3.5	543	5	ABV61361	ABV61361 Human ORF	230	30	3.5	2265	7	ACA80603	AcA80603 Human sec
158	30	3.5	565	3	AACT5891	AACT5891 Human ORF	231	30	3.5	2265	7	ACF19798	AcF19798 Human sec
159	30	3.5	659	3	AACT7234	AACT7234 Human ORF	232	30	3.5	2265	7	ACD21208	AcD21208 Human sec
160	30	3.5	669	6	ABQ75346	ABQ75346 Human bre	233	30	3.5	2265	7	ACD23554	AcD23554 Human sec
161	30	3.5	772	4	AA123666	AA123666 Human bre	234	30	3.5	2265	7	ACF00403	AcF00403 Human sec
162	30	3.5	791	6	ABT08076	ABT08076 Human bre	235	30	3.5	2265	7	ACA72460	AcA72460 Novel hum
163	30	3.5	805	4	AA196132	AA196132 Human neu	236	30	3.5	2265	7	ACD18445	AcD18445 Human sec
164	30	3.5	814	3	AAAF21759	AAAF21759 Human bre	237	30	3.5	2265	7		
165	30	3.5	816	7	ABT42385	ABT42385 Toxicity	238	30	3.5	2265	7		
166	30	3.5	817	6	ABL90239	ABL90239 Human pol	239	30	3.5	2265	7		
167	30	3.5	840	5	ABV04294	ABV04294 Human pro	240	30	3.5	2265	7		
168	30	3.5	846	4	AAFT4194	AAFT4194 DNA enco	241	30	3.5	2265	7		
169	30	3.5	868	5	ABV13463	ABV13463 Human pro	242	30	3.5	2265	7		

243	30	3.5	2265	7	ACD08452	Human	sec	316	30	3.5	2265	7	ACA91946	ACA91946	Human	PRO
244	30	3.5	2265	7	ACA88886	Novel	hum	317	30	3.5	2265	7	ACA71590	ACA71590	Human	sec
245	30	3.5	2265	7	ACA70328	Human	sec	318	30	3.5	2265	7	ACC09990	ACC09990	Human	sec
246	30	3.5	2265	7	ACD12550	Novel	hum	319	30	3.5	2265	7	ACA66000	ACA66000	CDNA	enco
247	30	3.5	2265	7	ACC74465	Human	sec	320	30	3.5	2265	7	ACA95145	ACA95145	CDNA	enco
248	30	3.5	2265	7	ACD16093	Human	sec	321	30	3.5	2265	7	ACD16707	ACD16707	Human	sec
249	30	3.5	2265	7	ACD25661	Novel	hum	322	30	3.5	2265	7	ACD15786	ACD15786	Human	sec
250	30	3.5	2265	7	ACD18138	Human	sec	323	30	3.5	2265	7	ABX16889	ABX16889	Human	CDN
251	30	3.5	2265	7	ACC88425	Human	sec	324	30	3.5	2265	7	ACA97830	ACA97830	Human	PRO
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258	30	3.5	2265	7	ACD21472	Human	sec	331	30	3.5	2265	8	ACF16628	ACF16628	Human	sec
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263	30	3.5	2265	7	ACD14514	Human	PRO	336	30	3.5	2265	8	ACF78217	ACF78217	Human	sec
264	30	3.5	2265	7	ACC91297	Human	sec	337	30	3.5	2265	8	ACD46922	ACD46922	Human	sec
265	30	3.5	2265	7	ACC89039	Human	sec	338	30	3.5	2265	8	ACD49685	ACD49685	Human	sec
266	30	3.5	2265	7	ACD07236	Human	PRO	339	30	3.5	2265	8	ACF28452	ACF28452	Human	sec
267	30	3.5	2265	7	ACA67687	Human	PRO	340	30	3.5	2265	8	ACD89142	ACD89142	Human	sec
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270	30	3.5	2265	7	ACC865702	Human	sec	343	30	3.5	2265	8	ADA78359	ADA78359	Human	sec
271	30	3.5	2265	7	ACC89990	Human	sec	344	30	3.5	2265	8	ACF49053	ACF49053	Human	sec
272	30	3.5	2265	7	ACC93139	Human	sec	345	30	3.5	2265	8	ACD09372	ACD09372	Human	sec
273	30	3.5	2265	7	ACA72767	Human	PRO	346	30	3.5	2265	8	ACF12166	ACF12166	Human	sec
274	30	3.5	2265	7	ACA92825	Human	sec	347	30	3.5	2265	8	ACF41400	ACF41400	Human	sec
275	30	3.5	2265	7	ACA70021	Human	sec	348	30	3.5	2265	8	ACF16014	ACF16014	Human	sec
276	30	3.5	2265	7	ACA97164	Novel	hum	349	30	3.5	2265	8	ACF16321	ACF16321	Human	sec
277	30	3.5	2265	7	ACA97160	Novel	hum	350	30	3.5	2265	8	ACD32148	ACD32148	Human	sec
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279	30	3.5	2265	7	ACA95452	Novel	hum	352	30	3.5	2265	8	ACF09403	ACF09403	Human	sec
280	30	3.5	2265	7	ACC86395	Human	sec	353	30	3.5	2265	8	ACF78524	ACF78524	Human	sec
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283	30	3.5	2265	7	ACF20105	Human	sec	356	30	3.5	2265	8	ACF24403	ACF24403	Human	sec
284	30	3.5	2265	7	ABX77049	Human	PRO	357	30	3.5	2265	8	ACF63714	ACF63714	Human	sec
285	30	3.5	2265	7	ACA73381	Novel	hum	358	30	3.5	2265	8	ACF50588	ACF50588	Human	sec
286	30	3.5	2265	7	ACA68924	Novel	hum	359	30	3.5	2265	8	ACH08059	ACH08059	Human	sec
287	30	3.5	2265	7	ACA74768	CDNA	enco	360	30	3.5	2265	8	ACF13865	ACF13865	Human	sec
288	30	3.5	2265	7	ACA70635	Human	sec	361	30	3.5	2265	8	ACD41791	ACD41791	Human	sec
289	30	3.5	2265	7	ACD14821	Human	PRO	362	30	3.5	2265	8	ACF32204	ACF32204	Human	sec
290	30	3.5	2265	7	ACA68493	Novel	hum	363	30	3.5	2265	8	ACF23482	ACF23482	Human	sec
291	30	3.5	2265	7	ABX88958	Novel	hum	364	30	3.5	2265	8	ACF40172	ACF40172	Human	sec
292	30	3.5	2265	7	ACC61435	Human	sec	365	30	3.5	2265	8	ACD45694	ACD45694	Human	sec
293	30	3.5	2265	7	ACA95759	Novel	hum	366	30	3.5	2265	8	ACF53351	ACF53351	Human	sec
294	30	3.5	2265	7	ACD04677	Novel	hum	367	30	3.5	2265	8	ACF27531	ACF27531	Human	sec
295	30	3.5	2265	7	ACC88118	Human	sec	368	30	3.5	2265	8	ACF45369	ACF45369	Human	sec
296	30	3.5	2265	7	ACF12780	Human	sec	369	30	3.5	2265	8	ACF29987	ACF29987	Human	sec
297	30	3.5	2265	7	ACA96495	Human	PRO	370	30	3.5	2265	8	ACD90063	ACD90063	Human	sec
298	30	3.5	2265	7	ACA55259	Human	PRO	371	30	3.5	2265	8	ACD84844	ACD84844	Human	PRO
299	30	3.5	2265	7	ACA73995	Human	sec	372	30	3.5	2265	8	ACD99004	ACD99004	CDNA	enco
300	30	3.5	2265	7	ACA74407	Novel	hum	373	30	3.5	2265	8	ACF77296	ACF77296	Human	sec
301	30	3.5	2265	7	ACA68802	Human	PRO	374	30	3.5	2265	8	ACF76989	ACF76989	Human	sec
302	30	3.5	2265	7	ACD10908	CDNA	enco	375	30	3.5	2265	8	ACF49974	ACF49974	Human	sec
303	30	3.5	2265	7	ACC91604	Human	sec	376	30	3.5	2265	8	ACF50281	ACF50281	Human	sec
304	30	3.5	2265	7	ACD02939	CDNA	enco	377	30	3.5	2265	8	ACD09680	ACD09680	Human	sec
305	30	3.5	2265	7	ACC87504	Human	sec	378	30	3.5	2265	8	ACD08759	ACD08759	Human	sec
306	30	3.5	2265	7	ACC86088	Human	sec	379	30	3.5	2265	8	ACF12473	ACF12473	Human	sec
307	30	3.5	2265	7	ACA65576	Human	PRO	380	30	3.5	2265	8	ACC94981	ACC94981	Human	sec
308	30	3.5	2265	7	ACA94393	Human	sec	381	30	3.5	2265	8	ACD22700	ACD22700	Human	sec
309	30	3.5	2265	7	ACA98137	Human	PRO	382	30	3.5	2265	8	ACF15400	ACF15400	Human	sec
310	30	3.5	2265	7	ACA91639	Novel	hum	383	30	3.5	2265	8	ACC97495	ACC97495	Human	sec
311	30	3.5	2265	7	ACA90853	Novel	hum	384	30	3.5	2265	8	ACC92525	ACC92525	Human	sec
312	30	3.5	2265	7	ACD16400	Human	sec	385	30	3.5	2265	8	ACF14172	ACF14172	Human	sec
313	30	3.5	2265	7	ACD17561	Human	sec	386	30	3.5	2265	8	ACF14479	ACF14479	Human	sec
314	30	3.5	2265	7	ACC92218	Human	sec	387	30	3.5	2265	8	ACF09710	ACF09710	Human	sec
315	30	3.5	2265	7	ACA75075	CDNA	enco	388	30	3.5	2265	8	ACD46001	ACD46001	Human	sec

389	3.5	2265	8	ACD48150	Human	sec	462	30	3.5	2265	8	ACH05241	CDNA	enco	ACH05241	CDNA	enco
390	3.5	2265	8	ACD67881	Human	enco	463	30	3.5	2265	8	ACH44738	Human	sec	ACH44738	Human	sec
391	3.5	2265	8	ACD55689	Human	sec	464	30	3.5	2265	8	ADA81878	Human	sec	ADA81878	Human	sec
392	3.5	2265	8	ACF29373	Human	sec	465	30	3.5	2265	8	ACD22393	Human	sec	ACD22393	Human	sec
393	3.5	2265	8	ACD85151	Human	sec	466	30	3.5	2265	8	ACD24740	Human	sec	ACD24740	Human	sec
394	3.5	2265	8	ACD84230	Human	sec	467	30	3.5	2265	8	ACD39943	CDNA	enco	ACD40250	CDNA	enco
395	3.5	2265	8	ACD88321	Human	sec	468	30	3.5	2265	8	ACD40250	CDNA	enco	ACD40250	CDNA	enco
396	3.5	2265	8	ACF30908	Human	sec	469	30	3.5	2265	8	ACF13558	Human	sec	ACF13558	Human	sec
397	3.5	2265	8	ACF32511	Human	sec	470	30	3.5	2265	8	ACF03360	Human	sec	ACF03360	Human	sec
398	3.5	2265	8	ACH12171	CDNA	enco	471	30	3.5	2265	8	ACF78831	Human	sec	ACF78831	Human	sec
399	3.5	2265	8	ACH12478	CDNA	enco	472	30	3.5	2265	8	ACF11552	Human	sec	ACF11552	Human	sec
400	3.5	2265	8	ACH12478	CDNA	enco	473	30	3.5	2265	8	ACF50895	Human	sec	ACF50895	Human	sec
401	3.5	2265	8	ACH18342	Human	sec	474	30	3.5	2265	8	ACF34330	Human	sec	ACF34330	Human	sec
402	3.5	2265	8	ACF08789	Human	sec	475	30	3.5	2265	8	ACD46515	Human	sec	ACD46515	Human	sec
403	3.5	2265	8	ACF31590	Human	sec	476	30	3.5	2265	8	ACD48457	Human	sec	ACD48457	Human	sec
404	3.5	2265	8	ACF52430	Human	sec	477	30	3.5	2265	8	ACF27838	Human	sec	ACF27838	Human	sec
405	3.5	2265	8	ACD50299	Human	sec	478	30	3.5	2265	8	ACF24710	Human	sec	ACF24710	Human	sec
406	3.5	2265	8	ACF39002	Human	sec	479	30	3.5	2265	8	ACD85765	Human	sec	ACD85765	Human	sec
407	3.5	2265	8	ACF26917	Human	sec	480	30	3.5	2265	8	ACD90370	Human	sec	ACD90370	Human	sec
408	3.5	2265	8	ACF25017	Human	sec	481	30	3.5	2265	8	ACD83923	Human	sec	ACD83923	Human	sec
409	3.5	2265	8	ACF46597	Human	sec	482	30	3.5	2265	8	ACF49360	Human	sec	ACF49360	Human	sec
410	3.5	2265	8	ACF28145	Human	sec	483	30	3.5	2265	8	ACH07445	Human	sec	ACH07445	Human	sec
411	3.5	2265	8	ACH089449	Human	sec	484	30	3.5	2265	8	ACH07752	Human	sec	ACH07752	Human	sec
412	3.5	2265	8	ACH64021	Human	sec	485	30	3.5	2265	8	ACH08366	Human	sec	ACH08366	Human	sec
413	3.5	2265	8	ACH60661	Human	sec	486	30	3.5	2265	8	ACH11557	CDNA	enco	ACH11557	CDNA	enco
414	3.5	2265	8	ACH12785	CDNA	enco	487	30	3.5	2265	8	ACH11864	Human	sec	ACH11864	Human	sec
415	3.5	2265	8	ACH10208	Human	sec	488	30	3.5	2265	8	ACH10515	Human	sec	ACH10515	Human	sec
416	3.5	2265	8	ACH04063	Human	sec	489	30	3.5	2265	8	ACH01518	Human	sec	ACH01518	Human	sec
417	3.5	2265	8	ACH10601	Human	sec	490	30	3.5	2265	8	ACH41093	Human	sec	ACH41093	Human	sec
418	3.5	2265	8	ACH42828	Human	sec	491	30	3.5	2265	8	ACD44433	Human	sec	ACD44433	Human	sec
419	3.5	2265	8	ACH18649	Human	sec	492	30	3.5	2265	8	ACH01534	Human	sec	ACH01534	Human	sec
420	3.5	2265	8	ACH02439	Human	sec	493	30	3.5	2265	8	ACH18035	Human	sec	ACH18035	Human	sec
421	3.5	2265	8	ACH21947	Human	sec	494	30	3.5	2265	8	ACH32818	Human	sec	ACH32818	Human	sec
422	3.5	2265	8	ACH10631	Human	sec	495	30	3.5	2265	8	ACH40479	Human	sec	ACH40479	Human	sec
423	3.5	2265	8	ACH34083	Human	sec	496	30	3.5	2265	8	ACH48439	Human	sec	ACH48439	Human	sec
424	3.5	2265	8	ACH45045	Human	sec	497	30	3.5	2265	8	ACH38388	Human	sec	ACH38388	Human	sec
425	3.5	2265	8	ACH90677	Human	sec	498	30	3.5	2265	8	ACH25324	Human	sec	ACH25324	Human	sec
426	3.5	2265	8	ACH91290	Human	sec	499	30	3.5	2265	8	ACH72224	Human	sec	ACH72224	Human	sec
427	3.5	2265	8	ACH30601	Human	sec	500	30	3.5	2265	8	ACH29680	Human	sec	ACH29680	Human	sec
428	3.5	2265	8	ACH87300	Human	sec	501	30	3.5	2265	8	ACH87914	Human	sec	ACH87914	Human	sec
429	3.5	2265	8	ACH660354	Human	sec	502	30	3.5	2265	8	ACH66375	Human	sec	ACH66375	Human	sec
430	3.5	2265	8	ACH466904	Human	sec	503	30	3.5	2265	8	ACH49667	Human	sec	ACH49667	Human	sec
431	3.5	2265	8	ACH75761	Human	sec	504	30	3.5	2265	8	ACH44124	Human	sec	ACH44124	Human	sec
432	3.5	2265	8	ACH80151	Human	sec	505	30	3.5	2265	8	ACH06469	Human	sec	ACH06469	Human	sec
433	3.5	2265	8	ACH17421	Human	sec	506	30	3.5	2265	8	ACH06776	CDNA	enco	ACH06776	CDNA	enco
434	3.5	2265	8	ACH23175	Human	sec	507	30	3.5	2265	8	ACH06776	CDNA	enco	ACH06776	CDNA	enco
435	3.5	2265	8	ACH08175	Human	sec	508	30	3.5	2265	8	ACH06776	CDNA	enco	ACH06776	CDNA	enco
436	3.5	2265	8	ACH08482	Human	sec	509	30	3.5	2265	8	ACH2832	Human	sec	ACH2832	Human	sec
437	3.5	2265	8	ACH40786	Human	sec	510	30	3.5	2265	8	ACH3446	Human	sec	ACH3446	Human	sec
438	3.5	2265	8	ACH53965	Human	sec	511	30	3.5	2265	8	ACH19481	Human	sec	ACH19481	Human	sec
439	3.5	2265	8	ACH47229	Human	sec	512	30	3.5	2265	8	ACH13182	Human	sec	ACH13182	Human	sec
440	3.5	2265	8	ACH47229	Human	sec	513	30	3.5	2265	8	ACH06640	Human	sec	ACH06640	Human	sec
441	3.5	2265	8	ACH48132	Human	sec	514	30	3.5	2265	8	ACH04674	Human	sec	ACH04674	Human	sec
442	3.5	2265	8	ACH47518	Human	sec	515	30	3.5	2265	8	ACH098102	Human	sec	ACH098102	Human	sec
443	3.5	2265	8	ACH46290	Human	sec	516	30	3.5	2265	8	ACH098102	Human	sec	ACH098102	Human	sec
444	3.5	2265	8	ACH86379	Human	sec	517	30	3.5	2265	8	ACH098102	Human	sec	ACH098102	Human	sec
445	3.5	2265	8	ACH52737	Human	sec	518	30	3.5	2265	8	ACH2321	Human	sec	ACH2321	Human	sec
446	3.5	2265	8	ACH53044	Human	sec	519	30	3.5	2265	8	ACH13297	Human	sec	ACH13297	Human	sec
447	3.5	2265	8	ACH65037	Human	sec	520	30	3.5	2265	8	ACH43256	CDNA	enco	ACH43256	CDNA	enco
448	3.5	2265	8	ACH76682	Human	sec	521	30	3.5	2265	8	ACH43563	CDNA	enco	ACH43563	CDNA	enco
449	3.5	2265	8	ACH61582	Human	sec	522	30	3.5	2265	8	ACH15093	Human	sec	ACH15093	Human	sec
450	3.5	2265	8	ACH61589	Human	sec	523	30	3.5	2265	8	ACH01825	Human	sec	ACH01825	Human	sec
451	3.5	2265	8	ACH30920	Human	sec	524	30	3.5	2265	8	ACH31897	Human	sec	ACH31897	Human	sec
452	3.5	2265	8	ACH31841	Human	sec	525	30	3.5	2265	8	ACH67574	CDNA	enco	ACH67574	CDNA	enco
453	3.5	2265	8	ACH32762	Human	sec	526	30	3.5	2265	8	ACH48764	Human	sec	ACH48764	Human	sec
454	3.5	2265	8	ACH17728	Human	sec	527	30	3.5	2265	8	ACH49071	Human	sec	ACH49071	Human	sec
455	3.5	2265	8	ACH07561	Human	sec	528	30	3.5	2265	8	ACH51509	Human	sec	ACH51509	Human	sec
456	3.5	2265	8	ACH20719	Human	sec	529	30	3.5	2265	8	ACH54272	Human	sec	ACH54272	Human	sec
457	3.5	2265	8	ACH21026	Human	sec	530	30	3.5	2265	8	ACH25996	Human	sec	ACH25996	Human	sec
458	3.5	2265	8	ACH21333	Human	sec	531	30	3.5	2265	8	ACH39309	Human	sec	ACH39309	Human	sec
459	3.5	2265	8	ACH47843	Human	sec	532	30	3.5	2265	8	ACH29066	Human	sec	ACH29066	Human	sec
460	3.5	2265	8	ACH47825	Human	sec	533	30	3.5	2265	8	ACH09093	Human	sec	ACH09093	Human	sec
461	3.5	2265	8	ACH36588	Human	sec	534	30	3.5	2265	8	ACH86686	Human	sec	ACH86686	Human	sec
				ACH105348	CDNA	enco						ACH05548	CDNA	enco			
				ACH86993	Human	sec						ACH65344	CDNA	enco			

535	30	3.5	2265	8	ADB20719	AdB20719	Human	sec	608	30	3.5	2265	8	ACD23007	AcD23007	Human	sec
536	30	3.5	2265	8	ACF43817	ACf43817	Human	sec	609	30	3.5	2265	8	ACF41707	ACf41707	Human	sec
537	30	3.5	2265	8	ACH09287	ACH09287	Human	sec	610	30	3.5	2265	8	ACF07254	ACf07254	Human	sec
538	30	3.5	2265	8	ACH09594	ACH09594	Human	sec	611	30	3.5	2265	8	ACF77910	ACf77910	Human	sec
539	30	3.5	2265	8	AdA78971	AdA78971	Human	sec	612	30	3.5	2265	8	ACD46308	ACd46308	Human	sec
540	30	3.5	2265	8	ACF10017	ACf10017	Human	sec	613	30	3.5	2265	8	ACF47211	ACf47211	Human	sec
541	30	3.5	2265	8	ACF51202	ACf51202	Human	sec	614	30	3.5	2265	8	ACF54579	ACf54579	Human	sec
542	30	3.5	2265	8	ACF24096	ACf24096	Human	sec	615	30	3.5	2265	8	ACF45983	ACf45983	Human	sec
543	30	3.5	2265	8	ACD88528	ACd88528	Human	sec	616	30	3.5	2265	8	ACF45676	ACf45676	Human	sec
544	30	3.5	2265	8	ACH09901	ACH09901	Human	sec	617	30	3.5	2265	8	ACF38695	ACf38695	Human	sec
545	30	3.5	2265	8	ACH10822	ACH10822	Human	sec	618	30	3.5	2265	8	ACD89756	ACd89756	Human	sec
546	30	3.5	2265	8	ACH11629	ACH11629	Human	sec	619	30	3.5	2265	8	ACD85458	ACd85458	Human	sec
547	30	3.5	2265	8	ACC96679	ACC96679	Human	sec	620	30	3.5	2265	8	ACD86072	ACd86072	Human	sec
548	30	3.5	2265	8	ACC98709	ACC98709	Human	sec	621	30	3.5	2265	8	ACF76068	ACf76068	Human	sec
549	30	3.5	2265	8	ACF42014	ACf42014	Human	sec	622	30	3.5	2265	8	ACF60968	ACf60968	Human	sec
550	30	3.5	2265	8	ACF16935	ACf16935	Human	sec	623	30	3.5	2265	8	ACH05855	ACH05855	cdna	enco
551	30	3.5	2265	8	ACD32455	ACd32455	Human	sec	624	30	3.5	2265	8	ADA83042	ADa83042	Human	sec
552	30	3.5	2265	8	ACD30613	ACd30613	Human	sec	625	30	3.5	2265	8	ACF56114	ACf56114	Human	sec
553	30	3.5	2265	8	ACD41484	ACd41484	Human	sec	626	30	3.5	2265	8	ACF55500	ACf55500	Human	sec
554	30	3.5	2265	8	ACF07868	ACf07868	Human	sec	627	30	3.5	2265	9	ADB86350	ADb86350	Human	sec
555	30	3.5	2265	8	ACF31283	ACf31283	Human	sec	628	30	3.5	2265	9	ACF56421	ACf56421	Human	sec
556	30	3.5	2265	8	ACF77603	ACf77603	Human	sec	629	30	3.5	2265	9	ACF56728	ACf56728	Human	sec
557	30	3.5	2265	8	ACF11245	ACf11245	Human	sec	630	30	3.5	2265	9	ACF55193	ACf55193	Human	sec
558	30	3.5	2265	8	ACF33125	ACf33125	Human	sec	631	30	3.5	2265	9	ACF55193	ACf55193	Human	sec
559	30	3.5	2265	8	ACF26303	ACf26303	Human	sec	632	30	3.5	2265	9	ADD06080	ADd06080	Human	sec
560	30	3.5	2265	8	ACD83616	ACd83616	Human	PRO	633	30	3.5	2265	9	ADD10632	ADd10632	Human	sec
561	30	3.5	2265	8	ACF23789	ACf23789	Human	sec	634	30	3.5	2265	9	ADD11592	ADd11592	Human	sec
562	30	3.5	2265	8	ACF43203	ACf43203	Human	sec	635	30	3.5	2265	9	ADD37385	ADd37385	Human	sec
563	30	3.5	2265	8	ACF43510	ACf43510	Human	sec	636	30	3.5	2265	10	ADB41593	ADb41593	Human	sec
564	30	3.5	2265	8	ACH06162	ACH06162	cdna	enco	637	30	3.5	2265	10	ADB74774	ADb74774	Human	sec
565	30	3.5	2265	8	ACH08980	ACH08980	Human	sec	638	30	3.5	2265	10	ADB75356	ADb75356	Human	sec
566	30	3.5	2265	8	ACC90574	ACC90574	Human	sec	639	30	3.5	2307	3	ACF77488	ACf77488	Human	ORF
567	30	3.5	2265	8	ACF10938	ACf10938	Human	sec	640	30	3.5	2329	5	AAAD17002	AAAd17002	Human	arg
568	30	3.5	2265	8	ACC93753	ACC93753	Human	sec	641	30	3.5	2613	9	ADB62364	ADb62364	Human	CDN
569	30	3.5	2265	8	ACC96372	ACC96372	Human	sec	642	30	3.5	2627	7	ADA83753	ADa83753	Human	ZNF
570	30	3.5	2265	8	ACD25047	ACd25047	Human	sec	643	30	3.5	2725	4	AAAF37048	AAAf37048	Human	PRO
571	30	3.5	2265	8	ACF02132	ACf02132	Human	sec	644	30	3.5	2725	4	AAAF54262	AAAf54262	Human	PRO
572	30	3.5	2265	8	ACF22254	ACf22254	Human	sec	645	30	3.5	2725	4	AAAD02922	AAAd02922	Human	CDN
573	30	3.5	2265	8	ACF22868	ACf22868	Human	sec	646	30	3.5	2725	4	AAAS21483	AAAs21483	Human	CDN
574	30	3.5	2265	8	ACF09096	ACf09096	Human	sec	647	30	3.5	2725	5	AAAC91482	AAAc91482	Human	PRO
575	30	3.5	2265	8	ACF33442	ACf33442	Human	sec	648	30	3.5	2725	5	ACD24092	ACd24092	Novel	hum
576	30	3.5	2265	8	ACF54886	ACf54886	Human	sec	649	30	3.5	2725	7	ACA67233	ACa67233	cdna	enco
577	30	3.5	2265	8	ACF48746	ACf48746	Human	sec	650	30	3.5	2725	7	ACA67233	ACa67233	cdna	enco
578	30	3.5	2265	8	ACD47536	ACd47536	Human	sec	651	30	3.5	2725	7	ACB38380	ACb38380	DNA	encoD
579	30	3.5	2265	8	ACD49378	ACd49378	Human	sec	652	30	3.5	2725	7	ABX89380	ABx89380	Human	DNA
580	30	3.5	2265	8	ACF38081	ACf38081	Human	sec	653	30	3.5	2725	7	ABX13478	ABx13478	Human	DNA
581	30	3.5	2265	8	ACF30294	ACf30294	Human	sec	654	30	3.5	2725	7	ACD42034	ACd42034	Human	sec
582	30	3.5	2265	8	ACD87607	ACd87607	Human	sec	655	30	3.5	2725	7	ACA04263	ACa04263	Human	CDN
583	30	3.5	2265	8	ACF62196	ACf62196	Human	sec	656	30	3.5	2725	8	ADA45998	ADa45998	Novel	hum
584	30	3.5	2265	8	ACH11129	ACH11129	Human	sec	657	30	3.5	2725	8	ADA76429	ADa76429	Human	PRO
585	30	3.5	2265	8	ACD10294	ACd10294	Human	sec	658	30	3.5	2725	8	ADA19079	ADa19079	Human	PRO
586	30	3.5	2265	8	ACD17019	ACd17019	cdna	enco	659	30	3.5	2725	8	ADA61702	ADa61702	Homo sapi	
587	30	3.5	2265	8	ACC99316	ACC99316	Human	sec	660	30	3.5	2725	8	ADB219487	ADb219487	Novel	hum
588	30	3.5	2265	8	ACF00710	ACf00710	Human	sec	661	30	3.5	2725	8	ADB28028	ADb28028	cdna	enco
589	30	3.5	2265	8	ACD41177	ACd41177	Human	sec	662	30	3.5	2725	8	ADA86507	ADa86507	Human	hum
590	30	3.5	2265	8	ACF44786	ACf44786	Human	sec	663	30	3.5	2725	8	ADB16071	ADb16071	Human	PRO
591	30	3.5	2265	8	ACF22561	ACf22561	Human	sec	664	30	3.5	2725	8	ADA47857	ADa47857	Human	PRO
592	30	3.5	2265	8	ACF11859	ACf11859	Human	sec	665	30	3.5	2725	8	ADA68299	ADa68299	Novel	hum
593	30	3.5	2265	8	ACF11859	ACf11859	Human	sec	666	30	3.5	2725	8	ADA67652	ADa67652	Human	PRO
594	30	3.5	2265	8	ACF51816	ACf51816	Human	sec	667	30	3.5	2725	8	ADB30659	ADb30659	cdna	enco
595	30	3.5	2265	8	ACF31739	ACf31739	Human	sec	668	30	3.5	2725	8	ADA85955	ADa85955	Novel	hum
596	30	3.5	2265	8	ACD49992	ACd49992	Human	sec	669	30	3.5	2725	8	ADA97167	ADa97167	Human	PRO
597	30	3.5	2265	8	ACF37774	ACf37774	Human	sec	670	30	3.5	2725	8	ADA79471	ADa79471	Human	PRO
598	30	3.5	2265	8	ACF28759	ACf28759	Human	sec	671	30	3.5	2725	8	ADA87610	ADa87610	Novel	hum
599	30	3.5	2265	8	ACD88835	ACd88835	Human	sec	672	30	3.5	2725	8	ADBI6812	ADBi6812	Human	PRO
600	30	3.5	2265	8	ACF75454	ACf75454	Human	sec	673	30	3.5	2725	8	ADA91904	ADa91904	Novel	hum
601	30	3.5	2265	8	ACF61275	ACf61275	Human	sec	674	30	3.5	2725	8	ADBI1967	ADBi1967	Human	PRO
602	30	3.5	2265	8	ACF44431	ACf44431	Human	sec	675	30	3.5	2725	8	ADA18928	ADa18928	Novel	hum
603	30	3.5	2265	8	ACH08673	ACH08673	Human	sec	676	30	3.5	2725	8	ADA94143	ADa94143	Human	PRO
604	30	3.5	2265	8	ACC94060	ACC94060	Human	sec	677	30	3.5	2725	8	ADB20039	ADb20039	Novel	hum
605	30	3.5	2265	8	ACD21165	ACd21165	Human	sec	678	30	3.5	2725	8	ADBI1351	ADBi1351	Human	PRO
606	30	3.5	2265	8	ACF06947	ACf06947	Human	sec	679	30	3.5	2725	8	ACD98663	ACd98663	Novel	hum
607	30	3.5	2265	8	ACD20858	ACd20858	Human	sec	680	30	3.5	2725	8	ADA74605	ADa74605	Human	PRO

681	30	3.5	2725	8	ADB24838	AdB24838	Human	PRO	754	30	3.5	2725	9	ADD04708	AdD04708	Novel	hum
682	30	3.5	2725	8	ADa82362	AdA82362	Human	PRO	755	30	3.5	2725	9	ADc80664	AdC80664	Novel	hum
683	30	3.5	2725	8	ADa75325	AdA75325	Human	PRO	756	30	3.5	2725	9	ADd11171	AdD11171	Human	PRO
684	30	3.5	2725	8	ADa85403	AdA85403	Novel	hum	757	30	3.5	2725	9	ADc48052	AdC48052	Human	PRO
685	30	3.5	2725	8	ADa84851	AdA84851	Novel	hum	758	30	3.5	2725	9	ADc80112	AdC80112	Novel	hum
686	30	3.5	2725	8	ADb30107	AdB30107	CDNA	enco	759	30	3.5	2725	9	ADd09581	AdD09581	Human	PRO
687	30	3.5	2725	8	ADa80635	AdA80635	Human	PRO	760	30	3.5	2725	9	ADd41294	AdD41294	Novel	hum
688	30	3.5	2725	8	ADa75877	AdA75877	Human	PRO	761	30	3.5	2725	9	ADd52433	AdD52433	CDNA	enco
689	30	3.5	2725	8	ADa47102	AdA47102	Human	PRO	762	30	3.5	2725	9	ADd15375	AdD15375	Novel	hum
690	30	3.5	2725	8	ADb25398	AdB25398	Human	PRO	763	30	3.5	2725	9	ADd70602	AdD70602	Human	CDN
691	30	3.5	2725	8	ADa93574	AdA93574	Human	PRO	764	30	3.5	2725	9	ADd39679	AdD39679	Human	CDN
692	30	3.5	2725	8	ADb26924	AdB26924	CDNA	enco	765	30	3.5	2725	9	ADd53173	AdD53173	CDNA	enco
693	30	3.5	2725	8	ADb31211	AdB31211	CDNA	enco	766	30	3.5	2725	9	ADd53725	AdD53725	Novel	hum
694	30	3.5	2725	8	ADa61139	AdA61139	Human	PRO	767	30	3.5	2725	9	ADd70125	AdD70125	Human	CDN
695	30	3.5	2725	8	ADb24886	AdB24886	Human	PRO	768	30	3.5	2725	9	ADd38246	AdD38246	Human	CDN
696	30	3.5	2725	8	ADa96615	AdA96615	Human	PRO	769	30	3.5	2725	9	ADd39202	AdD39202	Human	CDN
697	30	3.5	2725	8	ADa81187	AdA81187	Human	PRO	770	30	3.5	2725	9	ADd51881	AdD51881	CDNA	enco
698	30	3.5	2725	8	ADb26372	AdB26372	CDNA	enco	771	30	3.5	2725	9	ADd02680	AdD02680	Human	PRO
699	30	3.5	2725	8	ADb21857	AdB21857	Novel	hum	772	30	3.5	2725	9	ADd02114	AdD02114	Human	PRO
700	30	3.5	2725	8	ADa77636	AdA77636	Human	PRO	773	30	3.5	2725	9	ADd54296	AdD54296	Novel	hum
701	30	3.5	2725	8	ADb18376	AdB18376	CDNA	enco	774	30	3.5	2725	9	ADd38725	AdD38725	Human	CDN
702	30	3.5	2725	8	ADb18376	AdB18376	CDNA	enco	775	30	3.5	2725	9	ADd40156	AdD40156	Human	CDN
703	30	3.5	2725	8	ADa87059	AdA87059	Novel	hum	776	30	3.5	2725	9	ADd50377	AdD50377	Human	CDN
704	30	3.5	2725	8	ADa04401	AdA04401	Human	CDN	777	30	3.5	2725	9	ADd92613	AdD92613	Human	PRO
705	30	3.5	2725	8	ADa88162	AdA88162	Novel	hum	778	30	3.5	2725	9	ADd91509	AdD91509	Human	PRO
706	30	3.5	2725	8	ADa46550	AdA46550	Novel	hum	779	30	3.5	2725	9	ADdE04123	AdD04123	Human	PRO
707	30	3.5	2725	8	ADb28580	AdB28580	CDNA	enco	780	30	3.5	2725	9	ADdE19989	AdD19989	Human	CDN
708	30	3.5	2725	8	ADb29132	AdB29132	CDNA	enco	781	30	3.5	2725	9	ADdE32420	AdD32420	Novel	hum
709	30	3.5	2725	8	ADa77084	AdA77084	Human	PRO	782	30	3.5	2725	9	ADdE22352	AdD22352	CDNA	enco
710	30	3.5	2725	8	ADb67945	AdB67945	Novel	hum	783	30	3.5	2725	9	ADd79576	AdD79576	CDNA	enco
711	30	3.5	2725	8	ADa88714	AdA88714	Novel	hum	784	30	3.5	2725	9	ADdE42112	AdD42112	Human	PRO
712	30	3.5	2725	8	ADa97719	AdA97719	Novel	hum	785	30	3.5	2725	9	ADdE17929	AdD17929	Human	PRO
713	30	3.5	2725	8	ADb27476	AdB27476	CDNA	enco	786	30	3.5	2725	9	ADd92061	AdD92061	Human	PRO
714	30	3.5	2725	8	ADb22409	AdB22409	Novel	hum	787	30	3.5	2725	9	ADdE33524	AdD33524	Novel	hum
715	30	3.5	2725	8	ADa67100	AdA67100	Human	PRO	788	30	3.5	2725	9	ADdE34076	AdD34076	Novel	hum
716	30	3.5	2725	8	ADb22961	AdB22961	Human	PRO	789	30	3.5	2725	9	ADdE80128	AdD80128	CDNA	enco
717	30	3.5	2725	8	ADb23734	AdB23734	Human	PRO	790	30	3.5	2725	9	ADdE49900	AdD49900	Human	CDN
718	30	3.5	2725	8	ADb292456	AdB292456	Novel	hum	791	30	3.5	2725	9	ADd93165	AdD93165	Human	PRO
719	30	3.5	2725	8	ADb15519	AdB15519	Human	PRO	792	30	3.5	2725	9	ADdE19585	AdD19585	Human	PRO
720	30	3.5	2725	8	ADb38771	AdB38771	Novel	hum	793	30	3.5	2725	9	ADdE21458	AdD21458	Human	CDN
721	30	3.5	2725	8	ADb38219	AdB38219	Novel	hum	794	30	3.5	2725	9	ADdE19033	AdD19033	Human	PRO
722	30	3.5	2725	8	ADb66691	AdB66691	Novel	hum	795	30	3.5	2725	9	ADdE43229	AdD43229	Human	PRO
723	30	3.5	2725	8	ADb89771	AdB89771	Human	PRO	796	30	3.5	2725	9	ADdE96018	AdD96018	Human	PRO
724	30	3.5	2725	8	ADb39503	AdB39503	Human	PRO	797	30	3.5	2725	9	ADdE22804	AdD22804	CDNA	enco
725	30	3.5	2725	8	ADb39604	AdB39604	Novel	hum	798	30	3.5	2725	9	ADd79022	AdD79022	CDNA	enco
726	30	3.5	2725	8	ADb47227	AdB47227	Novel	hum	799	30	3.5	2725	9	ADdE32972	AdD32972	Novel	hum
727	30	3.5	2725	8	ADb86834	AdB86834	Human	PRO	800	30	3.5	2725	9	ADdE42664	AdD42664	Human	PRO
728	30	3.5	2725	8	ADb77439	AdB77439	Novel	hum	801	30	3.5	2725	9	ADdE80680	AdD80680	CDNA	enco
729	30	3.5	2725	8	ADb34596	AdB34596	Human	PRO	802	30	3.5	2725	9	ADdE89708	AdD89708	Human	PRO
730	30	3.5	2725	8	ADb35700	AdB35700	Human	PRO	803	30	3.5	2725	9	ADdE40992	AdD40992	Human	PRO
731	30	3.5	2725	8	ADb34044	AdB34044	Human	PRO	804	30	3.5	2725	9	ADdE04791	AdD04791	Human	PRO
732	30	3.5	2725	8	ADb35148	AdB35148	Human	PRO	805	30	3.5	2725	10	ADdE81216	AdD81216	Novel	hum
733	30	3.5	2725	8	ADb36252	AdB36252	Human	PRO	806	30	3.5	2725	10	ADd76664	AdD76664	Human	PRO
734	30	3.5	2725	8	ADb46647	AdB46647	Novel	hum	807	30	3.5	2725	10	ADdE88028	AdD88028	Human	PRO
735	30	3.5	2725	8	ADb17956	AdB17956	Human	PRO	808	30	3.5	2725	10	ADdE64332	AdD64332	Human	PRO
736	30	3.5	2725	8	ADc50520	AdC50520	Novel	hum	809	30	3.5	2725	10	ADdE75880	AdD75880	Human	PRO
737	30	3.5	2725	8	ADc72067	AdC72067	Novel	hum	810	30	3.5	2725	10	ADdE23456	AdD23456	Human	PRO
738	30	3.5	2725	8	ADc60046	AdC60046	Novel	hum	811	30	3.5	2725	10	ADdE24008	AdD24008	Human	PRO
739	30	3.5	2725	8	ADc59053	AdC59053	Novel	hum	812	30	3.5	2725	10	ADdE24651	AdD24651	Human	PRO
740	30	3.5	2725	8	ADc57407	AdC57407	Novel	hum	813	30	3.5	2725	10	ADdE87476	AdD87476	Human	PRO
741	30	3.5	2725	8	ADc60598	AdC60598	Novel	hum	814	30	3.5	2725	10	ADdE89342	AdD89342	Human	PRO
742	30	3.5	2725	8	ADc51073	AdC51073	Novel	hum	815	30	3.5	2725	10	ADdE18481	AdD18481	Human	PRO
743	30	3.5	2725	8	ADc65600	AdC65600	Human	PRO	816	30	3.5	2725	10	ADdE88790	AdD88790	Human	PRO
744	30	3.5	2725	8	ADc54698	AdC54698	Novel	hum	817	30	3.5	2725	6	ADdE28520	AdD28520	Human	PRO
745	30	3.5	2725	8	ADc53659	AdC53659	Novel	hum	818	30	3.5	2725	3	ADdA37087	AdD37087	Human	PRO
746	30	3.5	2725	8	ADc59182	AdC59182	Novel	hum	819	30	3.5	2725	4	ADdA53364	AdD53364	DNA	encod
747	30	3.5	2725	8	ADc56060	AdC56060	Novel	hum	820	30	3.5	2725	4	ADdA92106	AdD92106	Human	PRO
748	30	3.5	2725	8	ADc58630	AdC58630	Novel	hum	821	30	3.5	2725	6	ADdX33629	AdD33629	CDNA	enco
749	30	3.5	2725	8	ADd03304	AdD03304	Novel	hum	822	30	3.5	2725	6	ADdE74426	AdD74426	Human	CDN
750	30	3.5	2725	8	ADc90296	AdC90296	Novel	hum	823	30	3.5	2725	7	ADdA66934	AdD66934	CDNA	enco
751	30	3.5	2725	8	ADc69715	AdC69715	Novel	hum	824	30	3.5	2725	7	ADdE66686	AdD66686	Novel	hum
752	30	3.5	2725	8	ADc48604	AdC48604	Human	PRO	825	30	3.5	2725	7	ADdA91212	AdD91212	Human	PRO
753	30	3.5	2725	8	ADd10133	AdD10133	Human	PRO	826	30	3.5	2725	7	ADdE81589	AdD81589	Human	CDN

827	30	3.5	2848	7	ACA60411	Novel	hum	900	30	3.5	2848	10	ADC52235	Adc52235	Novel	hum	Adc52235	Novel	hum
828	30	3.5	2848	7	ACA58858	CDNA	enco	901	30	3.5	2848	10	ADC321061	Adc321061	Novel	hum	Adc321061	Novel	hum
829	30	3.5	2848	7	ACA64034	CDNA	enco	902	30	3.5	2848	10	AD505905	Ad505905	Human	PRO	Ad505905	Human	PRO
830	30	3.5	2848	7	ACA91298	CDNA	enco	903	30	3.5	2848	10	ADD75134	Add75134	Human	PRO	Add75134	Human	PRO
831	30	3.5	2848	7	ACD45197	Human	sec	904	30	3.5	2848	10	ADD75880	Add75880	Novel	hum	Add75880	Novel	hum
832	30	3.5	2848	7	ACA93745	Human	sec	905	30	3.5	2848	10	ADDB5118	Addb5118	Novel	hum	Addb5118	Novel	hum
833	30	3.5	2848	7	ACA67319	CDNA	enco	906	30	3.5	2848	10	ADDB6938	Addb6938	Novel	hum	Addb6938	Novel	hum
834	30	3.5	2848	7	ACA68590	Novel	hum	907	30	3.5	2848	10	ADDE0815	Adde0815	Novel	hum	Adde0815	Novel	hum
835	30	3.5	2848	7	ACH66292	Novel	hum	908	30	3.5	2848	10	ADDE39112	Adde39112	Novel	hum	Adde39112	Novel	hum
836	30	3.5	2848	7	ACD02346	Novel	hum	909	30	3.5	2848	10	AD505653	Ad505653	Human	PRO	Ad505653	Human	PRO
837	30	3.5	2848	7	ACA89337	Novel	hum	910	30	3.5	2848	10	ADD73644	Add73644	Human	PRO	Add73644	Human	PRO
838	30	3.5	2848	7	ACA68974	Novel	hum	911	30	3.5	2848	10	ADD78484	Add78484	Novel	hum	Add78484	Novel	hum
839	30	3.5	2848	7	ACA98496	Human	PRO	912	30	3.5	2848	10	ADDE21307	Adde21307	Novel	hum	Adde21307	Novel	hum
840	30	3.5	2848	7	ACA63421	CDNA	enco	913	30	3.5	2848	10	ADDE0569	Adde0569	Novel	hum	Adde0569	Novel	hum
841	30	3.5	2848	8	ABT44319	Human	PRO	914	30	3.5	2848	10	ADD75634	Add75634	Human	PRO	Add75634	Human	PRO
842	30	3.5	2848	8	ADB17154	Human	CDN	915	30	3.5	2848	10	ADD74150	Add74150	Human	PRO	Add74150	Human	PRO
843	30	3.5	2848	8	ACH03624	Human	sec	916	30	3.5	2848	10	ADD77810	Add77810	Novel	hum	Add77810	Novel	hum
844	30	3.5	2848	8	ACD68401	Novel	hum	917	30	3.5	2848	10	ADD76126	Add76126	Novel	hum	Add76126	Novel	hum
845	30	3.5	2848	8	ADA19959	Novel	hum	918	30	3.5	2848	10	ADDB85618	Addb85618	Novel	hum	Addb85618	Novel	hum
846	30	3.5	2848	8	ADB17342	Human	CDN	919	30	3.5	2848	10	ADDE05167	Adde05167	Human	PRO	Adde05167	Human	PRO
847	30	3.5	2848	8	ADBA20131	Novel	hum	920	30	3.5	2848	10	ADD75380	Add75380	Human	PRO	Add75380	Human	PRO
848	30	3.5	2848	8	ACD82138	Human	sec	921	30	3.5	2848	10	ADD76924	Add76924	Novel	hum	Add76924	Novel	hum
849	30	3.5	2848	8	ABT44602	Human	PRO	922	30	3.5	2848	10	ADDB6692-	Addb6692-	Novel	hum	Addb6692	Novel	hum
850	30	3.5	2848	8	ACD82269	Human	sec	923	30	3.5	2848	10	ADD78160	Add78160	Novel	hum	Add78160	Novel	hum
851	30	3.5	2848	8	ADA00428	Human	sec	924	30	3.5	2848	10	ADD77668	Add77668	Novel	hum	Add77668	Novel	hum
852	30	3.5	2848	8	ACH04503	Human	CDN	925	30	3.5	2848	10	ADD77914	Add77914	Novel	hum	Add77914	Novel	hum
853	30	3.5	2848	8	ACD68047	Novel	hum	926	30	3.5	2848	10	ADDB85372	Addb85372	Novel	hum	Addb85372	Novel	hum
854	30	3.5	2848	8	ABT43975	Novel	hum	927	30	3.5	2848	10	ADD73904	Add73904	Human	PRO	Add73904	Human	PRO
855	30	3.5	2848	8	ADDB85670	Novel	hum	928	30	3.5	2848	10	ADD77642	Add77642	Human	PRO	Add77642	Human	PRO
856	30	3.5	2848	8	ADB83677	Novel	hum	929	30	3.5	2848	10	ADD77170	Add77170	Novel	hum	Add77170	Novel	hum
857	30	3.5	2848	8	ADB80783	Novel	hum	930	30	3.5	2848	10	ADDB85864	Addb85864	Novel	hum	Addb85864	Novel	hum
858	30	3.5	2848	8	ADB73324	Novel	hum	931	30	3.5	2848	10	ADDB85864	Addb85864	Novel	hum	Addb85864	Novel	hum
859	30	3.5	2848	8	ADB78406	Novel	hum	932	30	3.5	2848	10	ADDE05413	Adde05413	Human	PRO	Adde05413	Human	PRO
860	30	3.5	2848	9	ADDB85054	Human	PRO	933	30	3.5	2848	10	ADD74888	Add74888	Human	PRO	Add74888	Human	PRO
861	30	3.5	2848	9	ADB78160	Novel	hum	934	30	3.5	2849	9	ADC17232	Adc17232	Novel	hum	Adc17232	Novel	hum
862	30	3.5	2848	9	ADB877226	Human	PRO	935	30	3.5	2849	9	ADC14930	Adc14930	Novel	hum	Adc14930	Novel	hum
863	30	3.5	2848	9	ADB84808	Human	PRO	936	30	3.5	2862	2	AAQ84612	AAq84612	Mouse	AT2	AAq84612	Mouse	AT2
864	30	3.5	2848	9	ADB68349	Human	PRO	937	30	3.5	2875	4	AAAD17208	AAad17208	Human	car	AAad17208	Human	car
865	30	3.5	2848	9	ADB68156	Human	PRO	938	30	3.5	2884	2	AAQ84613	AAq84613	Rat	AT2	AAq84613	Rat	AT2
866	30	3.5	2848	9	ADDB83923	Novel	hum	939	30	3.5	2917	4	AAQ67631	AAq67631	Human	ly1	AAq67631	Human	ly1
867	30	3.5	2848	9	ADB71078	Novel	hum	940	30	3.5	3200	2	AAAT07076	AAat07076	Cancer	su	AAat07076	Cancer	su
868	30	3.5	2848	9	ADB90873	Novel	hum	941	30	3.5	3489	7	AAQ51572	AAq51572	Human	str	AAq51572	Human	str
869	30	3.5	2848	9	ADC07053	Human	PRO	942	30	3.5	3716	7	AAQ51572	AAq51572	Human	str	AAq51572	Human	str
870	30	3.5	2848	9	ADC18097	Human	PRO	943	30	3.5	3583	5	AAQ24206	AAq24206	Human	NOV	AAq24206	Human	NOV
871	30	3.5	2848	9	ADC36916	Human	PRO	944	30	3.5	6303	5	AAQ85428	AAq85428	Human	net	AAq85428	Human	net
872	30	3.5	2848	9	ADC52425	Novel	hum	945	30	3.5	10004	5	ABBA14483	ABba14483	Human	DNA	ABba14483	Human	DNA
873	30	3.5	2848	9	ADC21906	Human	PRO	946	30	3.5	201143	6	AAQ02146	AAq02146	Human	sec	AAq02146	Human	sec
874	30	3.5	2848	9	ADC49937	Novel	hum	947	29	3.3	49	2	AAAT88080	AAat88080	3' portio		AAat88080	3' portio	
875	30	3.5	2848	9	ADC49136	Novel	hum	948	29	3.3	49	2	AAQ30225	AAq30225	CYP2D6	ge	AAq30225	CYP2D6	ge
876	30	3.5	2848	9	ADC49653	Novel	hum	949	29	3.3	49	6	AAQ54636	AAq54636	DNA	detec	AAq54636	DNA	detec
877	30	3.5	2848	9	ADC47514	Novel	hum	950	29	3.3	53	2	AAQ54636	AAq54636	DNA	detec	AAq54636	DNA	detec
878	30	3.5	2848	9	ADC47259	Novel	hum	951	29	3.3	56	6	AAQ54636	AAq54636	DNA	detec	AAq54636	DNA	detec
879	30	3.5	2848	9	ADC78134	Novel	hum	952	29	3.3	58	4	AAI29341	AAi29341	ColOn	tum	AAi29341	ColOn	tum
880	30	3.5	2848	9	ADDO6569	Novel	hum	953	29	3.3	58	6	AAQ55233	AAq55233	Human	col	AAq55233	Human	col
881	30	3.5	2848	9	ADC77888	Novel	hum	954	29	3.3	58	7	AAQ55233	AAq55233	Human	col	AAq55233	Human	col
882	30	3.5	2848	9	ADC77888	Novel	hum	955	29	3.3	64	6	AAQ55108	AAq55108	Human	col	AAq55108	Human	col
883	30	3.5	2848	9	ADC50851	Novel	hum	956	29	3.3	71	6	AAQ51039	AAq51039	GUS	mRNA	AAq51039	GUS	mRNA
884	30	3.5	2848	9	ADC51097	Novel	hum	957	29	3.3	74	6	AAQ51039	AAq51039	GUS	mRNA	AAq51039	GUS	mRNA
885	30	3.5	2848	9	ADC70743	Human	CDN	958	29	3.3	76	6	AAQ51039	AAq51039	GUS	mRNA	AAq51039	GUS	mRNA
886	30	3.5	2848	9	ADC39820	Human	CDN	959	29	3.3	76	6	AAQ51039	AAq51039	GUS	mRNA	AAq51039	GUS	mRNA
887	30	3.5	2848	9	ADC70266	Human	CDN	960	29	3.3	125	6	AAQ96267	AAq96267	Molecul	ar	AAq96267	Molecul	ar
888	30	3.5	2848	9	ADC36101	Novel	hum	961	29	3.3	132	3	AAQ49143	AAq49143	DNA	oligo	AAq49143	DNA	oligo
889	30	3.5	2848	9	ADC38387	Human	CDN	962	29	3.3	132	6	AAQ96172	AAq96172	Tumour	su	AAq96172	Tumour	su
890	30	3.5	2848	9	ADC50578	Human	PRO	963	29	3.3	140	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
891	30	3.5	2848	9	ADC50332	Human	PRO	964	29	3.3	148	6	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
892	30	3.5	2848	9	ADC38866	Human	CDN	965	29	3.3	150	6	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
893	30	3.5	2848	9	ADC40297	Human	CDN	966	29	3.3	156	7	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
894	30	3.5	2848	9	ADC51343	Novel	hum	967	29	3.3	160	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
895	30	3.5	2848	9	ADC50518	Human	CDN	968	29	3.3	167	2	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
896	30	3.5	2848	9	ADC50041	Human	CDN	969	29	3.3	190	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
897	30	3.5	2848	9	ADC21599	Human	CDN	970	29	3.3	200	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
898	30	3.5	2848	9	ADC48890	Novel	hum	971	29	3.3	202	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro
899	30	3.5	2848	10	ADC48890	Novel	hum	972	29	3.3	202	5	AAQ61179	AAq61179	Human	pro	AAq61179	Human	pro

abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 amino acid over production; herbicide resistance; glyphosate resistance;
 imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 porphyrin herbicide resistance; triazine resistance; disease resistance;
 modified oil production; modified starch production; waxy starch;
 altered floral morphology; male-sterile plant; albino mutant;
 modified fatty acid content; reduced palmitate production; albino plant;
 increased stearate production; reduced linolenic acid production;
 photosynthetic process.
 Malus x domestica.
 Synthetic.
 WO200192512-A2.
 06-DEC-2001.
 01-JUN-2001; 2001WO-US017672.
 01-JUN-2000; 2000US-0208538P;
 30-OCT-2000; 2000US-0244989P;
 27-MAR-2001; 2001US-00818875.
 (UYDE) UNIV DELAWARE.
 Kmiec EB, Gamper HB, Rice MC, Kim J;
 WPI; 2002-106307/14.
 New oligonucleotides with modified nuclease-resistant termini, useful for
 creating plants with desired phenotypes, e.g. stress tolerance, improved
 nutritional value, herbicide or disease resistance, or modified oil
 production.
 Claim 7; Page 91; 220pp; English.
 The invention relates to an oligonucleotide for targeted alteration of a
 genetic sequence, which comprises a single-stranded oligonucleotide
 having a DNA domain. The DNA domain has at least one mismatch with
 respect to the genetic sequence to be altered and further comprises
 chemical modifications of the oligonucleotide. The chemical modifications
 consist of o-methyl modification, an RNA modification, two or more
 phosphorothioate linkages on a terminus, or a combination of any two or
 more of these modifications. The oligonucleotides are useful for
 directing repair or alteration of plant genetic information. The
 oligonucleotides are particularly useful for creating plants with desired
 phenotypes, e.g. environmental or abiotic stress tolerance, improved
 nutritional value (e.g. altering amino acid content of plants or
 conferring amino acid over production), herbicide resistance (e.g.
 glyphosate resistance, imidazolinone and sulphonylurea herbicide
 resistance), porphyrin herbicide resistance or triazine resistance),
 disease resistance, modified oil production, modified starch production
 (e.g. increased starch or production of waxy starch), altered floral
 morphology (e.g. male-sterile plants) or modified fatty acid content
 (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 The oligonucleotides are also useful for producing albino mutants for the
 analysis of photosynthetic processes. This sequence represents a genome
 altering oligonucleotide of the invention
 Sequence 121 BP; 33 A; 29 C; 19 G; 40 T; 0 U; 0 Other;
 Query Match 8.1%; Score 70; DB 6; Length 121;
 Best Local Similarity 99.2%; Pred. No. 7.7e-18;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

148 A 148
 1 A 1
 Db
 RESULT 4
 ID ABK25466/c
 ABK25466 standard; DNA; 121 BP.
 AC
 XX
 DT 09-APR-2002 (first entry)
 DE Male-sterile plant producing genome altering oligonucleotide #366.
 XX
 XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KM o-methyl modification; RNA modification; phosphorothioate linkage;
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KM abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KM amino acid over production; herbicide resistance; glyphosate resistance;
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;
 KM modified oil production; modified starch production; waxy starch;
 KM altered floral morphology; male-sterile plant; albino mutant;
 KM modified fatty acid content; reduced palmitate production; albino plant;
 KM increased stearate production; reduced linolenic acid production;
 KM photosynthetic process.
 XX
 XX Malus x domestica.
 OS Synthetic.
 OS WO200192512-A2.
 PD 06-DEC-2001.
 PD 01-JUN-2001; 2001WO-US017672.
 PF 01-JUN-2000; 2000US-0208538P;
 PR 30-OCT-2000; 2000US-0244989P;
 PR 27-MAR-2001; 2001US-00818875.
 PA (UYDE) UNIV DELAWARE.
 PI Kmiec EB, Gamper HB, Rice MC, Kim J;
 WPI; 2002-106307/14.
 New oligonucleotides with modified nuclease-resistant termini, useful for
 creating plants with desired phenotypes, e.g. stress tolerance, improved
 nutritional value, herbicide or disease resistance, or modified oil
 production.
 Claim 7; Page 91; 220pp; English.
 The invention relates to an oligonucleotide for targeted alteration of a
 genetic sequence, which comprises a single-stranded oligonucleotide
 having a DNA domain. The DNA domain has at least one mismatch with
 respect to the genetic sequence to be altered and further comprises
 chemical modifications of the oligonucleotide. The chemical modifications
 consist of o-methyl modification, an RNA modification, two or more
 phosphorothioate linkages on a terminus, or a combination of any two or
 more of these modifications. The oligonucleotides are useful for
 directing repair or alteration of plant genetic information. The
 oligonucleotides are particularly useful for creating plants with desired
 phenotypes, e.g. environmental or abiotic stress tolerance, improved
 nutritional value (e.g. altering amino acid content of plants or
 conferring amino acid over production), herbicide resistance (e.g.
 glyphosate resistance, imidazolinone and sulphonylurea herbicide
 resistance), porphyrin herbicide resistance or triazine resistance),
 disease resistance, modified oil production, modified starch production
 (e.g. increased starch or production of waxy starch), altered floral
 morphology (e.g. male-sterile plants) or modified fatty acid content
 (e.g. reduced palmitate, increased stearate or reduced linolenic acid).

CC The invention relates to an oligonucleotide for targeted alteration of a

XX XX

PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNIV DELAMARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
XX
XX Claim 7; Page 90; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance), porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 40 A; 16 C; 41 G; 24 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 7.7e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGGAGCTGGAGGTTGATCAAGAGGATTGAGAACTCAAGTACAGGAGGTGACTTA 62
DB 1 GGGAGCTGGAGGTTGATCAAGAGGATTGAGAACTCAAGTACAGGAGGTGACTTA 60
QY 63 CTCCAAAGGAGGATGGATTATCAAGAGGAAAGGAGATCTCTGTTCTATGTATGC 122
DB 61 GTCCAAAGGAGGATGGATTATCAAGAGGAAAGGAGATCTCTGTTCTATGTATGC 120
QY 123 T 123
DB 121 T 121
RESULT 7
ABK25465
ID ABK25465 standard; DNA; 121 BP.
XX
XX ABK25465;
AC
XX 09-APR-2002 (first entry)
XX
XX Male-sterile plant producing genome altering oligonucleotide #365.
DE
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
XX o-methyl modification; LNA modification; phosphorothioate linkage;
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
XX abiotic stress tolerance; improved nutritional value; hygromycin; primer;

KM amino acid over production; herbicide resistance; glyphosate resistance;
KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KM porphyrin herbicide resistance; triazine resistance; disease resistance;
KM modified oil production; modified starch production; waxy starch;
KM altered floral morphology; male-sterile plant; albino mutant;
KM modified fatty acid content; reduced palmitate production; albino plant;
KM increased stearate production; reduced linolenic acid production;
KM photosynthetic process.
XX
XX Malus x domestica.
OS Synthetic.
XX
XX WO200192512-A2.
XX
XX 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US017672.
XX
XX 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNIV DELAMARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
XX
XX Claim 7; Page 91; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance), porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 39 A; 20 C; 28 G; 34 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 7.7e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 31 ATTGAACTCAAGTACAGGAGGAGTGCCTTACCTCAAGAGGAGGATGGATTATCAG 90
DB 1 ATTGAACTCAAGTACAGGAGGAGTGCCTTACCTCAAGAGGAGGATGGATTATCAG 60
QY 91 AAGGCAAGGAGATCACTGTTCTATGTATGATCTAAAGTATCTTATCATTTATTCAG 150
DB 61 TTGGCAAGGAGATCACTGTTCTATGTATGATCTAAAGTATCTTATCATTTATTCAG 120
QY 151 T 151

Db 121 T 121

RESULT 8
ABK25461
ID ABK25461 standard; DNA, 121 BP.
XX
XX
AC ABK25461;
XX
DT 09-APR-2002 (first entry)
DE Male-sterile plant producing genome altering oligonucleotide #361.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KM o-methyl modification; LNA modification; phosphorothioate linkage;
KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KM abiotic stress tolerance; improved nutritional value; hygromycin-B;
KM amino acid over production; herbicide resistance; glyphosate resistance;
KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KM porphyrin herbicide resistance; triazine resistance; disease resistance;
KM modified oil production; modified starch production; waxy starch;
KM altered floral morphology; male-sterile plant; albino mutant;
KM modified fatty acid content; reduced palmitate production; albino plant;
KM increased stearate production; reduced linolenic acid production;
KM photosynthetic process.
XX
XX Malus x domestica.
OS Synthetic.
XX
XX WO200192512-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 01-JUN-2001; 2001WO-US017672.
PF
XX
XX 01-JUN-2000; 2000US-0208538P.
PR
XX
XX 30-OCT-2000; 2000US-0244989P.
PR
XX
XX 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNITV DELAWARE.
XX
XX Kmiec EB, Gampier HB, Rice MC, Kim J;
PI
XX
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
PS
XX
XX Claim 7, Page 91; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance), porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the

CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
XX
SQ Sequence 121 BP, 40 A; 19 C; 29 G; 33 T; 0 U; 0 Other;
Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 7,7e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 28 AGATTAGAACTCTCACTAAGGCGAGTGACTCTCTCCAGAGGGAATGGATTATC 87
DB 1 AGGATTAGAACTCTCACTAAGGCGAGTGACTCTCTCCAGAGGGAATGGATTATC 60
OY 88 AAGAGGCAAGGAGATCTCTTCTATGATGCTTAAAGTATCTTATCATTTATCT 147
DB 61 TAGAGGCAAGGAGATCTCTTCTATGATGCTTAAAGTATCTTATCATTTATCT 120
OY 148 A 148
DB 121 A 121
RESULT 9
ABK25457
ID ABK25457 standard; DNA, 121 BP.
XX
XX
AC ABK25457;
XX
DT 09-APR-2002 (first entry)
DE Male-sterile plant producing genome altering oligonucleotide #357.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KM o-methyl modification; LNA modification; phosphorothioate linkage;
KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KM abiotic stress tolerance; improved nutritional value; hygromycin-B;
KM amino acid over production; herbicide resistance; glyphosate resistance;
KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KM porphyrin herbicide resistance; triazine resistance; disease resistance;
KM modified oil production; modified starch production; waxy starch;
KM altered floral morphology; male-sterile plant; albino mutant;
KM modified fatty acid content; reduced palmitate production; albino plant;
KM increased stearate production; reduced linolenic acid production;
KM photosynthetic process.
XX
XX Malus x domestica.
OS Synthetic.
XX
XX WO200192512-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 01-JUN-2001; 2001WO-US017672.
PF
XX
XX 01-JUN-2000; 2000US-0208538P.
PR
XX
XX 30-OCT-2000; 2000US-0244989P.
PR
XX
XX 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNITV DELAWARE.
XX
XX Kmiec EB, Gampier HB, Rice MC, Kim J;
PI
XX
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
PS
XX
XX Claim 7, Page 91; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide

CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of 0-methyl modification, an RNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes; e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 CC
 SQ Sequence 121 BP; 41 A; 17 C; 38 G; 25 T; 0 U; 0 Other;
 Query Match 8.1%; Score 70; DB 6; Length 121;
 Best Local Similarity 99.2%; Pred. No. 7.7e-16;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 CGTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGTGACTACTCC 66
 DB 1 CTTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGTGACTACTCC 60
 QY 67 AAGAGAGAGAAATGGGATTATCAAGAGGCAAGAGAGATCACTGTTATGTGATCTAAA 126
 DB 61 TAGAGAGAGAAATGGGATTATCAAGAGGCAAGAGAGATCACTGTTATGTGATCTAAA 120
 QY 127 G 127
 DB 121 G 121
 RESULT 10
 ID AAX27168 standard; DNA; 1964 BP.
 XX AAX27168;
 AC AAX27168;
 XX
 DT 27-MAY-1999 (first entry)
 XX
 DE Rat GMEB-2 coding sequence.
 XX
 KM GMEB-1, glucocorticoid modulating element binding protein;
 KM glucocorticoid receptor; GR dose-response curve; glucocorticoid hormone;
 KM rat; ss.
 XX
 OS Rattus norvegicus.
 XX
 PN WO9905273-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 14-JUL-1998; 98WO-US014423.
 XX
 PR 25-JUL-1997; 97US-0053846P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Simons SS, Kaul S, Jackson DA, Zeng H, Hiseaji O,
 XX
 DR WPI; 1999-153319/13.
 DR P-PSDB; AAY00894.
 XX
 PT New nucleic acid encoding glucocorticoid modulatory element binding
 PT protein - useful to increase the expression of genes that are linked to a

PT glucocorticoid modulatory element.
 XX
 PS Claim 2; Page 60-61; 78pp; English.
 XX
 CC This sequence encodes the rat glucocorticoid modulating element binding
 CC protein, GMEB-2, of the invention. The polypeptides interact with a GME
 CC (glucocorticoid modulatory element), linked to a nucleic acid sequence,
 CC resulting in increased expression of the nucleic acid sequence. The
 CC polypeptides may be supplied as such or provided by expression of the
 CC nucleic acid sequences, particularly to treat cells that do not produce
 CC sufficient, or functional, GME-binding protein. The nucleic acid
 CC sequences and the polypeptides of the invention can also be used to
 CC screen for presence of GME bound to a gene in a cell. Fragments of the
 CC nucleic acid sequences are useful as primers and probes to isolate the
 CC corresponding genomic sequence. The polypeptides may be used in two-
 CC hybrid screens to identify other proteins involved in modulating the
 CC glucocorticoid receptor (GR) dose-response curve. The polypeptides bind
 CC to GME, enhancing expression by a GR of a gene regulated by a GME
 CC (glucocorticoid responsive element). This results in increased expression
 CC of the GR-regulated gene (which may be endogenous or introduced by gene
 CC therapy) in presence of physiological levels of a glucocorticoid hormone
 CC
 SQ Sequence 1964 BP; 515 A; 539 C; 526 G; 384 T; 0 U; 0 Other;
 Query Match 3.9%; Score 34; DB 2; Length 1964;
 Best Local Similarity 100.0%; Pred. No. 0.00071;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 835 TTTTGGGAAAAA
 DB 1930 TTTTGGGAAAAA
 RESULT 11
 ID ADA02946
 XX ADA02946 standard; cDNA; 3130 BP.
 AC ADA02946;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Mouse Nk2 carcinoma associated cDNA, SEQ ID NO:1464.
 XX
 KM Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
 KM prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;
 KM gene; ss.
 XX
 OS Mus sp.
 XX
 PN WO2003057146-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041414.
 XX
 PR 26-DEC-2001; 2001US-00035832.
 XX
 PA (SAGR-) SAGRES DISCOVERY.
 XX
 PI Morris DW;
 XX
 DR WPI; 2003-587068/55.
 XX
 PT New recombinant nucleic acid encoding carcinoma associated protein,
 PT useful for preparing compositions for treating carcinomas.
 XX
 PS Claim 1; SEQ ID NO 1464; 245pp; English.
 XX
 CC The invention relates to recombinant carcinoma associated (CA) nucleic
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The
 CC invention also encompasses expression vectors and host cells comprising a
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically

CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC leukemia (especially breast cancer, prostate cancer, lymphoma or
CC leukemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed murine CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 8; Length 3130;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868

Db 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3117

RESULT 12

ADB72684
ID ADB72684 standard; mRNA; 3130 BP.

XX ADB72684;

XX 04-DEC-2003 (first entry)

DE Mouse Nek2 mRNA.

XX mouse; ss; cytosstatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma.

OS Mus sp.

XX WO2003008583-A2.

PN 30-JAN-2003.

XX 26-DEC-2001; 2001WO-US051291.

XX 02-MAR-2001; 2001US-00798586.

PR 23-OCT-2001; 2001US-00064113.

PR 08-NOV-2001; 2001US-00052482.

PR 30-NOV-2001; 2001US-00997722.

PR 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

PS Claim 1; SEQ ID NO 512; 2304bp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytosstatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and

CC sarcomas. The present sequence represents a mouse mRNA of the invention.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Seq Query Match 3.9%; Score 34; DB 9; Length 3130;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868

Db 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3117

RESULT 13

ADC85426
ID ADC85426 standard; DNA; 3130 BP.

XX ADC85426;

XX 01-JAN-2004 (first entry)

DE Mouse Nek2 mRNA sequence.

XX Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;

KM secreted; transmembrane; intracellular; ds.

OS Mus sp.

XX WO2003045230-A2.

XX 05-JUN-2003.

XX 02-DEC-2002; 2002WO-US038582.

XX 30-NOV-2001; 2001US-00997722.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-513603/48.

XX New recombinant nucleic acid comprising a nucleotide sequence of any of
PT the carcinoma-associated (CA) genes; useful for screening for drug
PT candidates for diagnosing or treating carcinomas.

PS Claim 1; SEQ ID NO 212; 983bp; English.

XX The invention relates to a recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the fully defined carcinoma-
CC associated (CA) genes from the 50 tables given in the specification. The
CC CA proteins are secreted, transmembrane or intracellular proteins. The
CC recombinant nucleic acids are useful for screening for drug candidates
CC for diagnosing or treating carcinomas. Sequences given in ADC85215-
CC ADC85514 represent CA genes of the invention.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 9; Length 3130;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868

Db 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3117

RESULT 14

ABL93464/C
ID ABL93464 standard; cDNA; 469 BP.

XX ABL93464;

XX

DT 10-JUN-2002 (first entry)
 XX Arabidopsis thaliana nucleic acid sequence Ref:2027229 SEQ ID NO:229.
 DE Arabidopsis thaliana, insecticide; fungicide; plant; mapping; diagnosis;
 XX genetic modification; gene; ss.
 KW Arabidopsis thaliana.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US200203280-A1.
 XX
 PD 21-FEB-2002.
 XX
 XX 26-JAN-2001; 2001US-00770444.
 PF
 XX 27-JAN-2000; 2000US-0178502P.
 PR
 XX (GORLACH J.
 PA (ANYI/ AN Y.
 PA (HAMIT/ HAMILTON C M.
 PA (PRIC/ PRICE J L.
 PA (RAIN/ RAINES T M.
 PA (YUY/ YU Y.
 PA (RAME/ RAMEAKA J G.
 PA (PAGE/ PAGE A.
 PA (MATH/ MATHW A V.
 PA (LEDF/ LEDFORD B L.
 PA (WOES/ WOESSNER J P.
 PA (HAAS/ HAAS W D.
 PA (GARC/ GARCIA C A.
 PA (KRIC/ KRICKER M.
 PA (SLAT/ SLATER T.
 PA (DAVI/ DAVIS K R.
 PA (ALLE/ ALLEN K.
 PA (HOFF/ HOFFMAN N.
 PA (HURB/ HURBAN P.
 XX
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,
 PI Hurban P;
 XX
 DR WPI: 2002-267486/31.
 XX
 XX New Arabidopsis thaliana nucleic acid, for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of a protein.
 XX
 PS Claim 1; SEQ ID NO 229; 44bp; English.
 XX
 CC The present invention describes an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridizing under stringent conditions
 CC to a sequence (SI) selected from any one of the 399 sequences given in
 CC ABL93236 to ABL94234. (I) have insecticide and fungicide activities, and
 CC they can be used as protein expression modulators. (I) can be used in
 CC identifying homologous or related genes, in producing compositions that
 CC modulate the expression or function of their encoded proteins, mapping
 CC functional regions of the proteins, and in studying associated
 CC physiological pathways. (I) can also be used: (1) for the genetic
 CC manipulation of cells, particularly plant cells; (2) in screening assays
 CC of various plant strains to determine the strains that are best capable
 CC of withstanding a particular disease or environmental stress; (3) for
 CC enhancing or inhibiting production of a biosynthetic product in a plant;
 CC (4) as probes in mapping and in diagnosis, in genetic modification and
 CC for screening purposes, to generate additional copies of the nucleic
 CC acids, to generate ribozymes or antisense oligonucleotides, and as single
 CC stranded DNA probes or as triple-strand forming oligonucleotides; and (5)
 CC for generating genetically modified transgenic organisms. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPRO web site
 XX
 SQ Sequence 469 BP; 120 A; 88 C; 93 G; 168 T; 0 U; 0 Other;

Query Match 3.8%; Score 33; DB 6; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 836 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868
 DB 65 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33
 RESULT 15
 ID AEX60840/C
 XX AEX60840 standard; DNA; 469 BP.
 AC AEX60840;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Arabidopsis thaliana polynucleotide #186.
 XX
 KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
 KW genetic modification; environmental stress; disease resistance;
 KW fungicide; insecticide; stress tolerance.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US2002142319-A1.
 XX
 PD 03-OCT-2002.
 XX
 XX 07-AUG-2001; 2001US-00924035.
 PF
 XX 13-AUG-1999; 99US-0148784P.
 PR 11-AUG-2000; 2000US-00638258.
 XX
 XX (GORLACH J.
 PA (ANYI/ AN Y.
 PA (HAMIT/ HAMILTON C M.
 PA (PRIC/ PRICE J L.
 PA (HARG/ HARGISS T R.
 PA (YUY/ YU Y.
 PA (RAME/ RAMEAKA J G.
 PA (PAGE/ PAGE A.
 PA (MATH/ MATHW A V.
 PA (LEDF/ LEDFORD B L.
 PA (WOES/ WOESSNER J P.
 PA (HAAS/ HAAS W D.
 PA (GARC/ GARCIA C A.
 XX
 XX Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y,
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA;
 XX
 DR WPI: 2003-102509/09.
 XX
 XX Novel Arabidopsis thaliana nucleic acid useful for constructing a
 PT transgenic plant with enhanced disease resistance and enhanced traits of
 PT interest, as probes, and in diagnosis and screening purposes.
 XX
 PS Claim 1; Page 67; 277bp; English.
 XX
 CC The invention relates to Arabidopsis thaliana nucleic acid sequences. The
 CC DNA sequences and the polypeptides they encode are useful for identifying
 CC homologous or related genes, for producing compositions that modulate the
 CC expression or function of the polypeptides, for mapping functional
 CC regions of the proteins, in diagnosis, for studying associated
 CC physiological pathways, for genetic manipulation of cells, preferably
 CC plant cells, in screening assays of various plant strains to determine
 CC the strains that are capable of withstanding a particular disease or
 CC environmental stress, for enhancing or inhibiting production of
 CC biosynthetic products in plants and to create genetically modified and
 CC transgenic organisms, such as plant cells and plants. Transgenic plants
 CC are useful for introducing or improving disease resistance and stress

CC tolerance in plants, screening biologically active agents, such as
 CC fungicides and insecticides, and for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial or medicinal value.
 CC Sequences ABX6065-ABX6154 represent Arabidopsis thaliana
 CC polynucleotides of the invention
 XX

SQ Sequence 469 BP; 120 A; 88 C; 93 G; 168 T; 0 U; 0 Other;

Query Match 3.8%; Score 33; DB 7; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 836 TTGTGGGAAAAAAAAAAAAAAAAAAAA 868
 Db 65 TTGTGGGAAAAAAAAAAAAAAAAAAAA 33

Search completed: September 25, 2004, 22:55:31
 Job time : 452.034 secs

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:02:32 ; Search time 3667.18 Seconds

(without alignments)
10259.034 Million cell updates/sec

Title: US-10-069-527-1

Perfect score: 868

Sequence: 1 atgggacgcggggaaggtcga.....aaaaaaaaaaaaaaaaaaaaa 868

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: gb_ba:*
2: gb_hvg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_str:*
28: em_un:*
29: em_vl:*
30: em_hvg_hum:*
31: em_hvg_inv:*
32: em_hvg_other:*
33: em_hvg_mus:*
34: em_hvg_pin:*
35: em_hvg_rtd:*
36: em_hvg_mam:*
37: em_hvg_vrt:*
38: em_sy:*
39: em_hvg_hum:*
40: em_hvg_mus:*
41: em_hvg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	868	100.0	868 8	MDO291490
2	691	79.6	890 8	AB081092
3	323	37.2	3130 8	MDO291491
4	70	8.1	121 6	AX324675
5	70	8.1	121 6	AX324676
6	70	8.1	121 6	AX324679
7	70	8.1	121 6	AX324680
8	70	8.1	121 6	AX324683
9	70	8.1	121 6	AX324684
10	70	8.1	121 6	AX324687
11	70	8.1	121 6	AX324688
12	36	4.1	1811 5	BC043631
13	34	3.9	967 8	AB038462
14	34	3.9	1929 9	BC043508
15	34	3.9	1964 10	AF059273
16	34	3.9	2572 9	HSM802300
17	34	3.9	3130 6	AX695837
18	34	3.9	3130 10	MMU95610
19	34	3.9	189394 2	AC115933
20	34	3.9	189394 2	AC115933
21	33	3.8	899 8	BYNCALMOD
22	33	3.8	110000 3	AC116957_1
23	33	3.8	179409 9	AC009831
24	33	3.8	182428 2	AC036167
25	33	3.8	213753 2	AC135743
26	32	3.7	597 5	AB033882
27	32	3.7	875 8	BPE48589
28	32	3.7	1067 9	BC005291
29	32	3.7	1350 9	BC007417
30	32	3.7	1399 9	BC047953
31	32	3.7	1811 9	BC036708
32	32	3.7	2324 9	BC039824
33	32	3.7	2600 10	BC037001
34	32	3.7	3575 9	BC030693
35	32	3.7	110000 2	AC098456_0
36	32	3.7	166073 2	AL772241
37	32	3.7	199337 2	BX649267
38	32	3.7	205964 2	AC145960
39	32	3.7	220420 5	BX000452
40	32	3.7	225764 2	AC133209
41	32	3.7	234502 2	BX322654
42	32	3.7	238530 5	BX539310
43	32	3.7	250264 2	AC108970
44	32	3.7	251762 3	AE014851
45	32	3.7	261251 2	AC098618
46	32	3.7	310779 2	AC005140
47	31	3.6	734 10	BC048516
48	31	3.6	784 10	BC031634
49	31	3.6	853 6	AX548546
50	31	3.6	964 6	189264
51	31	3.6	1013 9	BC002831
52	31	3.6	1065 5	GGNNANKX
53	31	3.6	1111 5	CGNKKX28
54	31	3.6	1111 6	AR213368
55	31	3.6	1136 10	BC048473
56	31	3.6	1246 6	AR213367
57	31	3.6	1257 6	AX478035
58	31	3.6	1333 8	AF268422
59	31	3.6	1358 9	AK026217
60	31	3.6	1416 10	RNMCHWR1
61	31	3.6	1536 8	AF190450
62	31	3.6	1540 10	BC037043
63	31	3.6	1604 8	AY465906
64	31	3.6	1803 10	BC025839
65	31	3.6	1808 6	AX535019

65	31	3.5	1897	9	BC002586	Homo sapi	139	30	3.5	763	9	BC003540	BC003540 Homo sapi
67	31	3.6	1898	10	BC031885	Mus muscu	140	30	3.5	763	9	BC009428	BC009428 Homo sapi
68	31	3.6	1951	9	BC027930	Homo sapi	141	30	3.5	803	10	AF169156	AF169156 Mus muscu
69	31	3.6	1953	9	AB053326	Homo sapi	142	30	3.5	805	6	BD019969	BD019969 Novel gen
70	31	3.6	1963	10	BC030492	Mus muscu	143	30	3.5	805	6	BD099907	BD099907 Novel gen
71	31	3.6	1988	9	AB053325	Homo sapi	144	30	3.5	816	10	AF402772	AF402772 Rattus no
72	31	3.6	1999	9	AB053324	Homo sapi	145	30	3.5	822	8	AB101439	AB101439 Prunus mu
73	31	3.6	2227	9	BC043620	Homo sapi	146	30	3.5	845	9	BC044653	BC044653 Homo sapi
74	31	3.6	2263	10	BC031747	Mus muscu	147	30	3.5	846	6	BD084043	BD084043 Homo sapi
75	31	3.6	2396	6	AX398420	Sequence	148	30	3.5	846	6	BD093358	BD093358 Enlironne
76	31	3.6	2714	6	AX358768	Sequence	149	30	3.5	879	8	AY428600	AY428600 Helianthu
77	31	3.6	2714	6	AX362261	Sequence	150	30	3.5	879	8	AY428600	AY428600 Helianthu
78	31	3.6	2714	6	AX358452	Homo sapi	151	30	3.5	912	3	AY069269	AY069269 Drosophil
79	31	3.6	2714	9	AY358452	Homo sapi	152	30	3.5	916	9	BC000308	BC000308 Homo sapi
80	31	3.6	3227	4	AF010191	Felis cat	153	30	3.5	916	9	BC019312	BC019312 Homo sapi
81	31	3.6	3227	4	AF010191	Felis cat	154	30	3.5	918	5	OMT580843	OMT580843 Oncothyrc
82	31	3.6	36148	3	AC116100	Dicyste	155	30	3.5	944	10	AF060872	AF060872 Mus muscu
83	31	3.6	49306	3	AC115606	Dicyste	156	30	3.5	952	3	AY0809308	AY0809308 Homo sapi
84	31	3.6	52867	2	AC021293	Homo sapi	157	30	3.5	952	3	AY089222	AY089222 Drosophil
85	31	3.6	137243	10	AL669902	Mouse DNA	158	30	3.5	965	10	BC046674	BC046674 Homo sapi
86	31	3.6	159034	2	BX470154	Danio rer	159	30	3.5	968	9	BC017116	BC017116 Homo sapi
87	31	3.6	160605	10	AC136101	Mus muscu	160	30	3.5	972	8	VURNACH14	VURNACH14 Mus muscu
88	31	3.6	161912	2	AC132314	Mus muscu	161	30	3.5	983	10	BC064085	BC064085 Mus muscu
89	31	3.6	167539	2	AC141812	Apis mell	162	30	3.5	983	10	AF154668	AF154668 Nicotiana
90	31	3.6	167539	2	AC141812	Apis mell	163	30	3.5	988	8	BD078441	BD078441 101 human
91	31	3.6	169092	2	AC027572	Homo sapi	164	30	3.5	990	6	BD078441	BD078441 101 human
92	31	3.6	177056	2	AC132579	Mus muscu	165	30	3.5	1018	3	AK113894	AK113894 Clona int
93	31	3.6	182709	2	AC108403	Mus muscu	166	30	3.5	1023	3	BC011708	BC011708 Homo sapi
94	31	3.6	190964	2	AC131772	Mus muscu	167	30	3.5	1037	8	AY046929	AY046929 Oryza sat
95	31	3.6	191118	2	AC133170	Mus muscu	168	30	3.5	1051	9	IR1034327	IR1034327 Homo sapi
96	31	3.6	197572	2	BX842704	Danio rer	169	30	3.5	1058	9	HSM800817	HSM800817 Homo sapi
97	31	3.6	200031	2	AC104676	Sus scrof	170	30	3.5	1068	9	HSM802823	HSM802823 Homo sapi
98	31	3.6	204652	2	PFMAL13P6	Plasmodiu	171	30	3.5	1068	9	AF002210	AF002210 Homo sapi
99	31	3.6	266115	2	AC122201	Mus muscu	172	30	3.5	1074	9	HSM800078	HSM800078 Homo sapi
100	31	3.6	307166	10	AC116748	Mus muscu	173	30	3.5	1076	3	MILEM1A	MILEM1A Homo sapi
101	30	3.5	79	6	AX494892	Sequence	174	30	3.5	1080	6	AR035137	AR035137 Sequence
102	30	3.5	160	6	AX494834	Sequence	175	30	3.5	1080	6	AR035137	AR035137 Sequence
103	30	3.5	166	6	AX494882	Sequence	176	30	3.5	1080	6	AR035137	AR035137 Sequence
104	30	3.5	169	6	AX494885	Sequence	177	30	3.5	1080	6	AR035137	AR035137 Sequence
105	30	3.5	197	6	AR425019	Sequence	178	30	3.5	1080	6	AR035137	AR035137 Sequence
106	30	3.5	197	6	BD120572	EST and e	179	30	3.5	1082	9	BC020940	BC020940 Homo sapi
107	30	3.5	198	6	AR425018	Sequence	180	30	3.5	1083	9	BC052605	BC052605 Homo sapi
108	30	3.5	198	6	BD120571	EST and e	181	30	3.5	1089	9	BC006505	BC006505 Homo sapi
109	30	3.5	217	6	AX182144	Sequence	182	30	3.5	1093	3	AF002571	AF002571 Homo sapi
110	30	3.5	380	11	BT028857	Sequence	183	30	3.5	1096	3	AF006727	AF006727 Meloidogy
111	30	3.5	412	5	LAU93207	Sequence	184	30	3.5	1101	9	BC001720	BC001720 Homo sapi
112	30	3.5	415	6	BD271551	49 human	185	30	3.5	1108	9	S62028	S62028 recoverin l
113	30	3.5	416	9	AK024545	Homo sapi	186	30	3.5	1109	10	BC031711	BC031711 Mus muscu
114	30	3.5	418	9	AK024545	Homo sapi	187	30	3.5	1135	9	BC026287	BC026287 Homo sapi
115	30	3.5	421	11	G15951	human SRS C	188	30	3.5	1144	9	AF014404	AF014404 Homo sapi
116	30	3.5	423	6	AX060654	Sequence	189	30	3.5	1178	9	BC014432	BC014432 Homo sapi
117	30	3.5	434	5	AF503957	Bp1nephel	190	30	3.5	1179	9	BC035797	BC035797 Homo sapi
118	30	3.5	451	6	AR415101	Sequence	191	30	3.5	1212	8	AY247801	AY247801 Arabidops
119	30	3.5	451	6	BD110654	EST and e	192	30	3.5	1218	9	AF117959	AF117959 Homo sapi
120	30	3.5	458	6	AX781005	Sequence	193	30	3.5	1226	9	AF052136	AF052136 Homo sapi
121	30	3.5	509	6	AY190740	Paqrus ma	194	30	3.5	1232	6	BD190855	BD190855 Secreted
122	30	3.5	520	6	AX386509	Sequence	195	30	3.5	1232	6	BD190855	BD190855 Secreted
123	30	3.5	522	9	AK026629	Homo sapi	196	30	3.5	1239	9	AK000852	AK000852 Homo sapi
124	30	3.5	529	9	BC003667	Homo sapi	197	30	3.5	1246	8	BT009439	BT009439 Homo sapi
125	30	3.5	572	6	AR174092	Sequence	198	30	3.5	1258	9	BC003557	BC003557 Homo sapi
126	30	3.5	572	6	BT009481	Sequence	199	30	3.5	1258	9	BC001894	BC001894 Homo sapi
127	30	3.5	608	10	BC048521	Mus muscu	200	30	3.5	1258	9	BC001894	BC001894 Homo sapi
128	30	3.5	609	9	BC020723	Homo sapi	201	30	3.5	1260	10	BC061808	BC061808 Rattus no
129	30	3.5	632	10	AB046449	Rattus no	202	30	3.5	1263	5	AF532312	AF532312 Opsanus b
130	30	3.5	634	11	BY032759	Sequence	203	30	3.5	1274	8	AY171231	AY171231 Chlamydom
131	30	3.5	669	9	AX523497	Sequence	204	30	3.5	1289	9	BC019268	BC019268 Homo sapi
132	30	3.5	681	9	AF028126	Homo sapi	205	30	3.5	1313	9	AY358200	AY358200 Homo sapi
133	30	3.5	685	9	AF293368	Homo sapi	206	30	3.5	1319	10	BC062057	BC062057 Mus muscu
134	30	3.5	710	9	BC063502	Homo sapi	207	30	3.5	1330	10	BC062057	BC062057 Mus muscu
135	30	3.5	737	10	AB046448	Mus muscu	208	30	3.5	1331	9	BC015524	BC015524 Homo sapi
136	30	3.5	742	9	AB046448	Mus muscu	209	30	3.5	1332	9	BC001055	BC001055 Homo sapi
137	30	3.5	744	9	AK074237	Homo sapi	210	30	3.5	1337	9	BC033871	BC033871 Homo sapi
138	30	3.5	751	9	AF229832	Homo sapi	211	30	3.5	1356	10	AF203914	AF203914 Mus muscu

212	30	3.5	1373	5	SACHORION	X93306 Sparus aur
213	30	3.5	1374	5	HSMB01163	AL117627 Homo sapi
214	30	3.5	1381	4	AB047244	AB047244 Sorex ung
215	30	3.5	1383	9	BC016792	BC016792 Homo sapi
216	30	3.5	1390	10	BC015307	BC015307 Mus muscu
217	30	3.5	1400	8	AY063461	AY063461 Helianthu
218	30	3.5	1411	6	AR177872	AR177872 Sequence
219	30	3.5	1416	6	AR340578	AR340578 Sequence
220	30	3.5	1414	6	AB5061	AB5061 Sequence 5
221	30	3.5	1414	6	AR316377	AR316377 Sequence
222	30	3.5	1414	6	BD058038	BD058038 Plants wi
223	30	3.5	1438	6	BC009834	BC009834 Homo sapi
224	30	3.5	1439	10	BC022734	BC022734 Mus muscu
225	30	3.5	1451	9	BC017400	BC017400 Homo sapi
226	30	3.5	1457	10	RNCKR5	Y12009 R.norvegicu
227	30	3.5	1469	10	BC005631	BC005631 Mus muscu
228	30	3.5	1485	9	AF159141	AF159141 Homo sapi
229	30	3.5	1512	9	BC003417	BC003417 Homo sapi
230	30	3.5	1546	9	BC023662	BC023662 Homo sapi
231	30	3.5	1552	9	AY358158	AY358158 Homo sapi
232	30	3.5	1562	5	BC045880	BC045880 Danio rer
233	30	3.5	1562	9	BC009879	BC009879 Homo sapi
234	30	3.5	1588	9	BC017012	BC017012 Homo sapi
235	30	3.5	1593	9	AF131792	AF131792 Homo sapi
236	30	3.5	1600	9	HSMB04708	HSMB04708 Homo sapi
237	30	3.5	1606	9	BC051328	BC051328 Homo sapi
238	30	3.5	1611	10	AF242858	AF242858 Mus muscu
239	30	3.5	1636	9	AY299331	AY299331 Homo sapi
240	30	3.5	1643	9	BC016979	BC016979 Homo sapi
241	30	3.5	1650	9	BC036976	BC036976 Homo sapi
242	30	3.5	1651	9	AB060282	AB060282 Macaca fa
243	30	3.5	1668	9	BC026038	BC026038 Homo sapi
244	30	3.5	1674	9	HSMB01259	AL122102 Homo sapi
245	30	3.5	1680	10	BC010314	BC010314 Mus muscu
246	30	3.5	1684	9	BC034406	BC034406 Homo sapi
247	30	3.5	1684	10	BC055910	BC055910 Mus muscu
248	30	3.5	1686	9	BC029879	BC029879 Homo sapi
249	30	3.5	1690	6	AX534999	AX534999 Sequence
250	30	3.5	1715	9	BC035857	BC035857 Homo sapi
251	30	3.5	1732	9	HSMB06891	BSX60874 Homo sapi
252	30	3.5	1747	5	BC057247	BC057247 Danio rer
253	30	3.5	1749	9	AK026164	AK026164 Homo sapi
254	30	3.5	1765	9	BC012891	BC012891 Homo sapi
255	30	3.5	1788	9	HSMB06673	BSX60627 Homo sapi
256	30	3.5	1805	9	BC026223	BC026223 Homo sapi
257	30	3.5	1821	5	AY095313	AY095313 Xenopus 1
258	30	3.5	1823	10	BC049889	BC049889 Mus muscu
259	30	3.5	1840	10	AF182714	AF182714 Rattus no
260	30	3.5	1846	10	BC047211	BC047211 Mus muscu
261	30	3.5	1848	5	XLCTCUD2	Y10075 X.laevi's m
262	30	3.5	1848	9	BC046357	BC046357 Homo sapi
263	30	3.5	1853	9	AF177331	AF177331 Homo sapi
264	30	3.5	1856	9	BC044250	BC044250 Homo sapi
265	30	3.5	1861	9	AK026830	AK026830 Homo sapi
266	30	3.5	1863	9	BC018654	BC018654 Homo sapi
267	30	3.5	1863	9	BC018654	BC018654 Homo sapi
268	30	3.5	1865	10	BC013463	BC013463 Mus muscu
269	30	3.5	1892	9	AB070011	AB070011 Macaca fa
270	30	3.5	1898	9	BC033207	BC033207 Homo sapi
271	30	3.5	1910	9	AF258548	AF258548 Homo sapi
272	30	3.5	1933	9	AB060850	AB060850 Macaca fa
273	30	3.5	1956	9	HSMB04748	AL833435 Homo sapi
274	30	3.5	1964	9	BC021799	BC021799 Homo sapi
275	30	3.5	1982	10	BC063088	BC063088 Mus muscu
276	30	3.5	1995	9	BC024685	BC024685 Mus muscu
277	30	3.5	1997	9	BC007210	BC007210 Homo sapi
278	30	3.5	2004	17	AF119860	AF119860 Homo sapi
279	30	3.5	2015	6	BD136416	BD136416 95 human
280	30	3.5	2021	10	AF188712	AF188712 Mus muscu
281	30	3.5	2036	8	HTU9756	AU009756 Helianthu
282	30	3.5	2042	9	HSMB01184	AL117647 Homo sapi
283	30	3.5	2077	9	BC048271	BC048271 Homo sapi
284	30	3.5	2080	10	BC064006	BC064006 Mus muscu
285	30	3.5	2102	10	BC029065	BC029065 Mus muscu
286	30	3.5	2116	9	BC050523	BC050523 Homo sapi
287	30	3.5	2131	9	BC034410	BC034410 Homo sapi
288	30	3.5	2132	9	AF258577	AF258577 Homo sapi
289	30	3.5	2152	10	AB000113	AB000113 Rattus no
290	30	3.5	2192	9	AK074246	AK074246 Homo sapi
291	30	3.5	2199	9	BC021851	BC021851 Homo sapi
292	30	3.5	2202	3	AK116052	AK116052 Ciona int
293	30	3.5	2228	9	BC062614	BC062614 Homo sapi
294	30	3.5	2240	9	AK000532	AK000532 Homo sapi
295	30	3.5	2265	6	AX376540	AX376540 Sequence
296	30	3.5	2265	6	AX454758	AX454758 Sequence
297	30	3.5	2265	6	AX491236	AX491236 Sequence
298	30	3.5	2265	9	AY359025	AY359025 Homo sapi
299	30	3.5	2265	9	BC014923	BC014923 Homo sapi
300	30	3.5	2286	9	BC020211	BC020211 Homo sapi
301	30	3.5	2290	9	BC015738	BC015738 Homo sapi
302	30	3.5	2314	9	BC050454	BC050454 Homo sapi
303	30	3.5	2326	3	AY119078	AY119078 Drosophi
304	30	3.5	2353	8	AF502079	AF502079 Glycine m
305	30	3.5	2353	9	BC032645	BC032645 Homo sapi
306	30	3.5	2355	9	AF250859	AF250859 Homo sapi
307	30	3.5	2358	9	BC017169	BC017169 Homo sapi
308	30	3.5	2364	3	AY122239	AY122239 Drosophi
309	30	3.5	2379	6	AX239965	AX239965 Sequence
310	30	3.5	2396	3	AF020407	AF020407 Dictyoste
311	30	3.5	2405	9	BC002881	BC002881 Homo sapi
312	30	3.5	2446	17	AF119856	AF119856 Homo sapi
313	30	3.5	2452	8	AB058413	AB058413 Chlamydom
314	30	3.5	2591	5	AK026213	AK026213 Homo sapi
315	30	3.5	2605	5	BC044351	BC044351 Danio rer
316	30	3.5	2613	6	AX746993	AX746993 Sequence
317	30	3.5	2613	9	AK091454	AK091454 Homo sapi
318	30	3.5	2627	6	AX676842	AX676842 Sequence
319	30	3.5	2718	9	BC008725	BC008725 Homo sapi
320	30	3.5	2725	6	AX055454	AX055454 Sequence
321	30	3.5	2725	6	AX089944	AX089944 Sequence
322	30	3.5	2725	6	AX464346	AX464346 Sequence
323	30	3.5	2725	6	AX697019	AX697019 Sequence
324	30	3.5	2725	9	AY358592	AY358592 Homo sapi
325	30	3.5	2731	10	BC037696	BC037696 Mus muscu
326	30	3.5	2749	9	HSMB02734	AL356155 Homo sapi
327	30	3.5	2772	9	AF357970	AF357970 Homo sapi
328	30	3.5	2796	5	AB070629	AB070629 Paratricht
329	30	3.5	2815	9	BC023597	BC023597 Homo sapi
330	30	3.5	2817	9	BC029104	BC029104 Homo sapi
331	30	3.5	2837	5	BC046834	BC046834 Xenopus 1
332	30	3.5	2841	10	BC014295	BC014295 Mus muscu
333	30	3.5	2846	9	HSMB02834	AL440282 Homo sapi
334	30	3.5	2848	6	AX092366	AX092366 Sequence
335	30	3.5	2848	6	AX358934	AX358934 Sequence
336	30	3.5	2848	6	AX362427	AX362427 Sequence
337	30	3.5	2848	6	AX697160	AX697160 Sequence
338	30	3.5	2848	9	AY358911	AY358911 Homo sapi
339	30	3.5	2862	6	I26126	I26126 Sequence 1
340	30	3.5	2862	10	S67465	S67465 angiofensin
341	30	3.5	2875	6	AX247632	AX247632 Sequence
342	30	3.5	2884	6	I26127	I26127 Sequence 5
343	30	3.5	2917	9	BC007609	BC007609 Homo sapi
344	30	3.5	2930	9	BC035395	BC035395 Homo sapi
345	30	3.5	2948	10	BC058100	BC058100 Mus muscu
346	30	3.5	2961	9	BC041128	BC041128 Homo sapi
347	30	3.5	2964	9	AK000622	AK000622 Homo sapi
348	30	3.5	3049	9	AK130506	AK130506 Homo sapi
349	30	3.5	3144	5	BC046266	BC046266 Xenopus 1
350	30	3.5	3200	6	A52563	A52563 Sequence 1
351	30	3.5	3200	6	I10222	I10222 CDNA of a t
352	30	3.5	3200	6	I26205	I26205 Sequence 1
353	30	3.5	3200	6	BC068884	BC068884 Homo sapi
354	30	3.5	3320	9	BC0077129	BC0077129 Mus muscu
355	30	3.5	3375	10	BC020166	BC020166 Homo sapi
356	30	3.5	3476	9	AF319949	AF319949 Mus muscu
357	30	3.5	3491	10		

358	3.5	3566	10	BC058990	BC058990 Mus muscu	431	3.5	145353	2	AC034177	AC034177 Homo sapi
359	3.5	3615	10	AF109143	AF109143 Mus muscu	432	3.5	145965	2	AC120216	AC120216 Mus muscu
360	3.5	3619	5	BC063897	BC063897 Siluana	433	3.5	146455	2	AC127512	AC127512 Homo sapi
361	3.5	3789	9	HSB081485	AL133620 Homo sapi	434	3.5	146690	2	AC102254	AC102254 Mus muscu
362	3.5	3799	9	BC044907	BC044907 Homo sapi	435	3.5	146877	2	AC026487	AC026487 Homo sapi
363	3.5	3813	9	BC042906	BC042906 Homo sapi	436	3.5	147265	2	AC116806	AC116806 Mus muscu
364	3.5	3813	9	BC061883	BC061883 Homo sapi	437	3.5	147489	2	AP001926	AP001926 Homo sapi
365	3.5	4073	10	BC057371	BC057371 Mus muscu	438	3.5	150442	2	AC022782	AC022782 Mus muscu
366	3.5	4543	9	BC054518	BC054518 Homo sapi	439	3.5	150810	2	AL954570	AL954570 Datto rer
367	3.5	4547	10	BC050875	BC050875 Mus muscu	440	3.5	150986	2	AC023802	AC023802 Mus muscu
368	3.5	4659	10	AF507918	AF507918 Mus muscu	441	3.5	151751	10	EX088539	EX088539 Mus muscu
369	3.5	4859	9	BC053676	BC053676 Homo sapi	442	3.5	152249	2	AC132874	AC132874 Mus muscu
370	3.5	4893	10	BC058105	BC058105 Mus muscu	443	3.5	152533	2	AC016506	AC016506 Homo sapi
371	3.5	5089	9	HSB080903	BC448942 Homo sapi	444	3.5	154055	2	AL157774	AL157774 Human DNA
372	3.5	6003	10	AY428535	AY428535 Mus muscu	445	3.5	154495	2	AC127223	AC127223 Mus muscu
373	3.5	7200	3	AF030197	AF030197 Drosophila	446	3.5	154685	10	AL606511	AL606511 Mouse DNA
374	3.5	18166	2	PF048196	AL929364 Plasmodiu	447	3.5	155586	2	AC115815	AC115815 Mus muscu
375	3.5	38181	2	AP005596	AP005596 Homo sapi	448	3.5	155752	10	EX539342	EX539342 Mus muscu
376	3.5	42188	10	AL929497	AL929497 Mouse DNA	449	3.5	156441	2	AC122106	AC122106 Rattus no
377	3.5	42188	2	AC101010	AC101010 Mus muscu	450	3.5	157455	2	AC131994	AC131994 Mus muscu
378	3.5	55041	2	AC099912	AC099912 Homo sapi	451	3.5	157662	2	AC011574	AC011574 Homo sapi
379	3.5	57250	2	AC083997	AC083997 Mus muscu	452	3.5	157676	2	AC027358	AC027358 Homo sapi
380	3.5	59364	2	AC102347	AC102347 Mus muscu	453	3.5	157676	2	AC027358	AC027358 Homo sapi
381	3.5	64227	2	AC100013	AC100013 Mus muscu	454	3.5	158195	2	AC101830	AC101830 Mus muscu
382	3.5	65691	3	PF048196	Z97348 Plasmodiu	455	3.5	158382	2	AC016507	AC016507 Homo sapi
383	3.5	73190	2	AC130416	AC130416 Homo sapi	456	3.5	158505	2	PF048196	PF048196 Plasmodiu
384	3.5	74586	2	AC060793	AC060793 Homo sapi	457	3.5	159505	2	AC023142	AC023142 Homo sapi
385	3.5	89128	8	NGB11823	AL669991 Neurospor	458	3.5	160149	2	AC118692	AC118692 Mus muscu
386	3.5	89251	9	AP001826	AP001826 Homo sapi	459	3.5	161247	2	AC111052	AC111052 Mus muscu
387	3.5	92636	5	AL603747	AL603747 Zebrafish	460	3.5	162061	2	AC069858	AC069858 Homo sapi
388	3.5	92636	5	AL603747	AL603747 Zebrafish	461	3.5	163216	2	AC122557	AC122557 Mus muscu
389	3.5	96095	4	BK640585	BK640585 Pig DNA s	462	3.5	163435	2	AC122432	AC122432 Homo sapi
390	3.5	100061	2	AC1019740	AC1019740 Homo sapi	463	3.5	164649	2	AC122378	AC122378 Mus muscu
391	3.5	1006418	9	AL355979	AL355979 Human DNA	464	3.5	167185	2	AC080108	AC080108 Homo sapi
392	3.5	106423	2	AC108692	AC108692 Homo sapi	465	3.5	167262	2	EX323810	EX323810 Datto rer
393	3.5	110000	2	AC111021	AC111021 Homo sapi	466	3.5	167835	2	AC120501	AC120501 Rattus no
394	3.5	110000	2	AC115630	AC115630 Homo sapi	467	3.5	167835	2	AC128859	AC128859 Rattus no
395	3.5	110000	2	AC115630	AC115630 Homo sapi	468	3.5	167858	2	EX555606	EX555606 Mus muscu
396	3.5	110000	2	EX255276	EX255276 Homo sapi	469	3.5	167858	2	AC011966	AC011966 Homo sapi
397	3.5	110000	2	EX255276	EX255276 Homo sapi	470	3.5	168447	2	AC115890	AC115890 Mus muscu
398	3.5	110000	2	BK470178	BK470178 Datto rer	471	3.5	168447	2	AC107676	AC107676 Mus muscu
399	3.5	110000	2	BK470178	BK470178 Datto rer	472	3.5	168804	2	AC009408	AC009408 Homo sapi
400	3.5	110000	2	PF048196	PF048196 Plasmodiu	473	3.5	169765	2	AC108109	AC108109 Homo sapi
401	3.5	110000	2	PF048196	PF048196 Plasmodiu	474	3.5	170569	2	AL228814	AL228814 Rattus no
402	3.5	110000	2	PF048196	PF048196 Plasmodiu	475	3.5	170569	2	AP001263	AP001263 Homo sapi
403	3.5	110000	2	PF048196	PF048196 Plasmodiu	476	3.5	170569	2	AC119889	AC119889 Mus muscu
404	3.5	110000	2	PF048196	PF048196 Plasmodiu	477	3.5	171590	2	AC119889	AC119889 Mus muscu
405	3.5	110000	2	PF048196	PF048196 Plasmodiu	478	3.5	171590	2	HS215K18	HS215K18 Human DNA s
406	3.5	110000	2	PF048196	PF048196 Plasmodiu	479	3.5	171936	2	AC120031	AC120031 Homo sapi
407	3.5	110000	2	PF048196	PF048196 Plasmodiu	480	3.5	172332	2	AC132843	AC132843 Mus muscu
408	3.5	110000	2	PF048196	PF048196 Plasmodiu	481	3.5	172424	2	AC114342	AC114342 Mus muscu
409	3.5	110000	2	PF048196	PF048196 Plasmodiu	482	3.5	172424	2	AC099628	AC099628 Mus muscu
410	3.5	110000	2	PF048196	PF048196 Plasmodiu	483	3.5	174470	10	AC114820	AC114820 Mus muscu
411	3.5	110000	2	PF048196	PF048196 Plasmodiu	484	3.5	174631	2	AC069059	AC069059 Homo sapi
412	3.5	110000	2	PF048196	PF048196 Plasmodiu	485	3.5	174631	2	AC069059	AC069059 Homo sapi
413	3.5	110000	2	PF048196	PF048196 Plasmodiu	486	3.5	174740	10	AL929086	AL929086 Zebrafish
414	3.5	110685	2	AL672211	AL672211 Human DNA	487	3.5	174740	10	AL929086	AL929086 Zebrafish
415	3.5	115898	2	AL672211	AL672211 Human DNA	488	3.5	175131	2	AC124806	AC124806 Mus muscu
416	3.5	119616	2	AL672211	AL672211 Human DNA	489	3.5	175260	2	AC119361	AC119361 Homo sapi
417	3.5	119820	2	HSB069H2	AL109330 Human DNA	490	3.5	175590	2	AC027119	AC027119 Homo sapi
418	3.5	120513	2	AC142244	AC142244 Mus muscu	491	3.5	176233	2	AC102885	AC102885 Mus muscu
419	3.5	123844	2	AC124673	AC124673 Mus muscu	492	3.5	176233	2	AC140556	AC140556 Didephus
420	3.5	124842	8	AC121236	AC121236 Medicago	493	3.5	176983	2	AC019172	AC019172 Homo sapi
421	3.5	124842	8	AC122163	AC122163 Medicago	494	3.5	177730	2	AC087844	AC087844 Homo sapi
422	3.5	130829	2	AC131706	AC131706 Mus muscu	495	3.5	178271	10	AC091785	AC091785 Genomic s
423	3.5	131943	2	AC005484	AC005484 Homo sapi	496	3.5	178875	2	AP001567	AP001567 Homo sapi
424	3.5	135862	10	AC135576	AC135576 Mus muscu	497	3.5	179249	2	AC129489	AC129489 Homo sapi
425	3.5	137009	9	AC009970	AC009970 Homo sapi	498	3.5	179249	2	AC129489	AC129489 Homo sapi
426	3.5	138710	10	AC023608	AC023608 Mus muscu	499	3.5	179416	2	AC140335	AC140335 Mus muscu
427	3.5	139097	2	AC004591	AC004591 Mus muscu	500	3.5	180392	2	AC019299	AC019299 Homo sapi
428	3.5	140233	10	AC136915	AC136915 Mus muscu	501	3.5	180978	2	AC067861	AC067861 Homo sapi
429	3.5	142616	2	AC028646	AC028646 Homo sapi	502	3.5	181179	9	AL161725	AL161725 Human DNA
430	3.5	144949	2	AC040935	AC040935 Homo sapi	503	3.5	181261	10	AC132346	AC132346 Mus muscu

504	3.5	181597	9	AC090515	AC090515 Homo sapi	577	3.5	208315	2	EX323864	EX323864 Danio rer
505	3.5	181597	9	AC090515	AC090515 Homo sapi	578	3.5	208342	2	AC105077	AC105077 Mus muscu
506	3.5	181805	10	AL670660	AL670660 Mouse DNA	579	3.5	208367	2	EX682542	EX682542 Mus muscu
507	3.5	182631	2	AC117661	AC117661 Mus muscu	580	3.5	208725	2	AC113302	AC113302 Mus muscu
508	3.5	182741	2	AC112855	AC112855 Rattus no	581	3.5	210013	2	AC130672	AC130672 Mus muscu
509	3.5	182870	3	AC116960	AC116960 Dictyoste	582	3.5	210390	2	AC110247	AC110247 Mus muscu
510	3.5	183046	2	AC140775	AC140775 Mus muscu	583	3.5	210501	2	AC131708	AC131708 Mus muscu
511	3.5	183997	2	AC126420	AC126420 Mus muscu	584	3.5	211041	2	AC116413	AC116413 Mus muscu
512	3.5	184480	10	AL928623	AL928623 Mouse DNA	585	3.5	211897	2	AC118500	AC118500 Rattus no
513	3.5	185286	2	AC119901	AC119901 Mus muscu	586	3.5	212485	10	AC090122	AC090122 Mus muscu
514	3.5	186846	2	AC091046	AC091046 Homo sapi	587	3.5	213171	2	AC119856	AC119856 Mus muscu
515	3.5	187700	2	AC131061	AC131061 Mus muscu	588	3.5	214395	10	AL831778	AL831778 Mouse DNA
516	3.5	187816	2	AC114404	AC114404 Mus muscu	589	3.5	214961	2	AC073473	AC073473 Homo sapi
517	3.5	188196	2	EX510911	EX510911 Danio rer	590	3.5	214962	2	AC123354	AC123354 Rattus no
518	3.5	188648	2	AC091266	AC091266 Mus muscu	591	3.5	214315	2	AC109231	AC109231 Mus muscu
519	3.5	188717	2	CNS01266	AL138478 Human chr	592	3.5	213992	2	AF002750	AF002750 Homo sapi
520	3.5	188768	9	AC023844	AC023844 Homo sapi	593	3.5	213379	2	AC124719	AC124719 Mus muscu
521	3.5	189378	2	AC023844	AC023844 Homo sapi	594	3.5	215941	2	AC124758	AC124758 Mus muscu
522	3.5	189334	2	AC124820	AC124820 Mus muscu	595	3.5	217002	2	AC121532	AC121532 Mus muscu
523	3.5	189356	9	AC005746	AC005746 Homo sapi	596	3.5	217015	10	AC117644	AC117644 Mus muscu
524	3.5	189880	5	EX248330	EX248330 Zebrafish	597	3.5	217351	2	AC103492	AC103492 Rattus no
525	3.5	190440	10	AC068252	AC068252 Mus muscu	598	3.5	218161	2	AC120871	AC120871 Mus muscu
526	3.5	191109	2	AC123683	AC123683 Mus muscu	599	3.5	218553	2	AC079940	AC079940 Mus muscu
527	3.5	191111	9	AC010282	AC010282 Homo sapi	600	3.5	218893	2	AC131687	AC131687 Mus muscu
528	3.5	191358	2	AC012533	AC012533 Homo sapi	601	3.5	219288	2	AC111912	AC111912 Rattus no
529	3.5	191673	2	AL356743	AL356743 Homo sapi	602	3.5	219903	2	AC098309	AC098309 Rattus no
530	3.5	191723	2	AC123627	AC123627 Mus muscu	603	3.5	219952	2	AC084804	AC084804 Mus muscu
531	3.5	191775	2	AC074358	AC074358 Mus muscu	604	3.5	220292	2	AC104743	AC104743 Mus muscu
532	3.5	192501	2	PEMALL3P1	AL049180 Plasmodiu	605	3.5	222205	2	AC125036	AC125036 Mus muscu
533	3.5	192582	2	AC093352	AC093352 Mus muscu	606	3.5	223089	2	AC129077	AC129077 Mus muscu
534	3.5	194138	2	AC131270	AC131270 Homo sapi	607	3.5	224031	10	AL844161	AL844161 Mouse DNA
535	3.5	194265	9	AC126365	AC126365 Homo sapi	608	3.5	224275	2	EX511189	EX511189 Danio rer
536	3.5	194274	2	AC147248	AC147248 Mus muscu	609	3.5	224513	2	AC090123	AC090123 Mus muscu
537	3.5	194303	2	AC115034	AC115034 Mus muscu	610	3.5	225320	2	AC114571	AC114571 Mus muscu
538	3.5	194449	2	AC103673	AC103673 Mus muscu	611	3.5	225383	2	AC108827	AC108827 Mus muscu
539	3.5	194695	2	AC026375	AC026375 Mus muscu	612	3.5	225870	2	AC099595	AC099595 Mus muscu
540	3.5	194871	9	CNS01266	AL118558 Human chr	613	3.5	225883	2	AC130017	AC130017 Rattus no
541	3.5	194912	2	EX005377	EX005377 Danio rer	614	3.5	226010	2	AC120559	AC120559 Rattus no
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543	3.5	195460	2	EX005307	EX005307 Rattus no	616	3.5	226898	2	AC098510	AC098510 Rattus no
544	3.5	195802	2	AC139160	AC139160 Rattus no	617	3.5	227458	2	AC110137	AC110137 Rattus no
545	3.5	196693	2	EX571706	EX571706 Danio rer	618	3.5	228767	5	EX005261	EX005261 Zebrafish
546	3.5	196882	2	AC027054	AC027054 Homo sapi	619	3.5	229535	2	AC130110	AC130110 Mus muscu
547	3.5	196890	2	AC137902	AC137902 Mus muscu	620	3.5	229762	2	AC102082	AC102082 Mus muscu
548	3.5	197430	2	AC140273	AC140273 Mus muscu	621	3.5	229904	2	AC115053	AC115053 Mus muscu
549	3.5	197450	2	AC140273	AC140273 Mus muscu	622	3.5	230188	2	AC091604	AC091604 Mus muscu
550	3.5	197662	2	AC024726	AC024726 Homo sapi	623	3.5	230254	2	AC074163	AC074163 Mus muscu
551	3.5	198687	2	EX813307	EX813307 Mus muscu	624	3.5	231177	2	AC121497	AC121497 Mus muscu
552	3.5	198767	2	AC116847	AC116847 Mus muscu	625	3.5	231546	2	EX784031	EX784031 Danio rer
553	3.5	199632	2	AC101885	AC101885 Mus muscu	626	3.5	231830	2	AC111010	AC111010 Mus muscu
554	3.5	199861	2	AC140419	AC140419 Mus muscu	627	3.5	232972	2	AC093991	AC093991 Rattus no
555	3.5	199919	2	EX547935	EX547935 Danio rer	628	3.5	233009	2	AC131686	AC131686 Mus muscu
556	3.5	200098	2	AC091161	AC091161 Homo sapi	629	3.5	233242	10	AL591070	AL591070 Mouse DNA
557	3.5	200146	2	AC115736	AC115736 Mus muscu	630	3.5	233487	2	AC134622	AC134622 Mus muscu
558	3.5	200292	2	AL929238	AL929238 Mus muscu	631	3.5	234810	2	AC105654	AC105654 Rattus no
559	3.5	201014	2	AC134595	AC134595 Mus muscu	632	3.5	234973	10	AC128850	AC128850 Mus muscu
560	3.5	201143	2	HS150C2	AL022318 Human DNA	633	3.5	235054	2	AC114393	AC114393 Rattus no
561	3.5	201479	10	AL848495	AL848495 Mouse DNA	634	3.5	235068	2	AC121721	AC121721 Rattus no
562	3.5	202027	2	AC120196	AC120196 Gallus ga	635	3.5	237187	10	AC116493	AC116493 Mus muscu
563	3.5	202316	10	AC138134	AC138134 Mus muscu	636	3.5	237547	2	EX539339	EX539339 Mus muscu
564	3.5	202521	2	AC146953	AC146953 Pongo pyg	637	3.5	237566	2	AC140384	AC140384 Mus muscu
565	3.5	203765	2	AC139635	AC139635 Gallus ga	638	3.5	237785	2	AC113970	AC113970 Mus muscu
566	3.5	204057	10	AL592283	AL592283 Mouse DNA	639	3.5	237894	2	AC123616	AC123616 Mus muscu
567	3.5	204278	10	AC124507	AC124507 Mus muscu	640	3.5	238408	2	AC140402	AC140402 Mus muscu
568	3.5	204990	2	AC024914	AC024914 Mus muscu	641	3.5	239352	2	AC106294	AC106294 Rattus no
569	3.5	205379	2	EX548050	EX548050 Danio rer	642	3.5	240332	2	AC118446	AC118446 Rattus no
570	3.5	205784	10	AC122891	AC122891 Mus muscu	643	3.5	242227	2	AC126064	AC126064 Rattus no
571	3.5	205893	10	AC084324	AC084324 Mus muscu	644	3.5	242777	2	AC102363	AC102363 Mus muscu
572	3.5	206419	2	AC127551	AC127551 Mus muscu	645	3.5	242949	2	AC116255	AC116255 Rattus no
573	3.5	207418	9	AC090774	AC090774 Homo sapi	646	3.5	243955	5	EX005070	EX005070 Zebrafish
574	3.5	207428	2	AC068605	AC068605 Mus muscu	647	3.5	243177	2	AC137437	AC137437 Rattus no
575	3.5	207431	10	AL589596	AL589596 Mouse DNA	648	3.5	243948	2	AC141896	AC141896 Mus muscu
576	3.5	208006	2	AC087877	AC087877 Mus muscu	649	3.5	245104	2	AC128348	AC128348 Rattus no

796	29	3.3	1043	10	BC028852	BC028852 Mus muscu	869	29	3.3	1522	5	AY178797	AY178797 Dantio rer
797	29	3.3	1050	9	BC039529	BC039529 Homo sapi	870	29	3.3	1528	9	BC010660	BC010660 Homo sapi
798	29	3.3	1064	8	AT091509	U91509 Arabidopsi	871	29	3.3	1534	9	AF237772	AF237772 Homo sapi
799	29	3.3	1064	10	BC047212	BC047212 Mus muscu	872	29	3.3	1549	9	BC013614	BC013614 Homo sapi
800	29	3.3	1068	10	BC004682	BC004682 Mus muscu	873	29	3.3	1563	9	AK026353	AK026353 Homo sapi
801	29	3.3	1075	3	AK114882	AK114882 Clona lnt	874	29	3.3	1564	9	AK024804	AK024804 Homo sapi
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803	29	3.3	1123	6	196163	196163 Sequence 2	876	29	3.3	1570	6	AX012186	AX012186 Sequence
804	29	3.3	1126	9	AF278737	AF278737 Actus ara	877	29	3.3	1570	6	BD226376	BD226376 Pancreati
805	29	3.3	1128	9	BC048811	BC048811 Homo sapi	878	29	3.3	1570	9	BC047022	BC047022 Homo sapi
806	29	3.3	1139	10	BC058435	BC058435 Mus muscu	879	29	3.3	1574	10	BC026387	BC026387 Mus muscu
807	29	3.3	1145	10	BC039656	BC039656 Mus muscu	880	29	3.3	1575	9	BC002643	BC002643 Homo sapi
808	29	3.3	1146	9	HSW802966	AL713744 Homo sapi	881	29	3.3	1593	9	BC035716	BC035716 Homo sapi
809	29	3.3	1153	10	BC058112	BC058112 Mus muscu	882	29	3.3	1609	8	AB070757	AB070757 Vigna ang
810	29	3.3	1155	10	AY036116	AY036116 Mus muscu	883	29	3.3	1614	5	BC056793	BC056793 Dantio rer
811	29	3.3	1159	6	BD269309	BD269309 33 human	884	29	3.3	1620	8	AF049930	AF049930 Petunia x
812	29	3.3	1163	9	AB049910	AB049910 Macaca fa	885	29	3.3	1625	9	BC004314	BC004314 Homo sapi
813	29	3.3	1166	8	AF076955	AF076955 Zea mays	886	29	3.3	1627	10	BC011174	BC011174 Mus muscu
814	29	3.3	1174	10	BC049559	BC049559 Mus muscu	887	29	3.3	1641	9	AF051325	AF051325 Homo sapi
815	29	3.3	1195	8	AF185574	AF185574 Populus t	888	29	3.3	1641	9	BC011575	BC011575 Homo sapi
816	29	3.3	1200	5	BD269287	BD269287 33 human	889	29	3.3	1651	9	BC012107	BC012107 Homo sapi
817	29	3.3	1209	5	BC062526	BC062526 Dantio rer	890	29	3.3	1656	9	BC017379	BC017379 Homo sapi
818	29	3.3	1224	10	BC040081	BC040081 Mus muscu	891	29	3.3	1661	10	BC003872	BC003872 Mus muscu
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825	29	3.3	1274	9	BC035847	BC035847 Homo sapi	898	29	3.3	1677	8	BPE490176	BPE490176 Betula pe
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832	29	3.3	1330	10	BC061713	BC061713 Rattus no	905	29	3.3	1680	8	BPE490292	BPE490292 Betula pe
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837	29	3.3	1353	9	BC013408	BC013408 Homo sapi	910	29	3.3	1683	8	BPE490286	BPE490286 Betula pe
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839	29	3.3	1394	10	BC011677	BC011677 Mus muscu	912	29	3.3	1693	10	BC040425	BC040425 Mus muscu
840	29	3.3	1395	10	BC002094	BC002094 Mus muscu	913	29	3.3	1711	8	AY061965	AY061965 Zea mays
841	29	3.3	1405	9	BC044934	BC044934 Homo sapi	914	29	3.3	1712	5	BC045320	BC045320 Dantio rer
842	29	3.3	1407	9	BC010409	BC010409 Homo sapi	915	29	3.3	1713	9	BC002798	BC002798 Homo sapi
843	29	3.3	1421	10	BC061257	BC061257 Mus muscu	916	29	3.3	1714	5	BC003655	BC003655 Homo sapi
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845	29	3.3	1429	9	BC008090	BC008090 Homo sapi	918	29	3.3	1731	3	AY118660	AY118660 Drosophi
846	29	3.3	1429	9	BC002088	BC002088 Homo sapi	919	29	3.3	1739	6	BD186888	BD186888 Nucleic a
847	29	3.3	1429	9	BC0044895	BC0044895 Homo sapi	920	29	3.3	1743	10	BC055837	BC055837 Mus muscu
848	29	3.3	1433	9	BC002539	BC002539 Homo sapi	921	29	3.3	1745	6	AR203358	AR203358 Sequence
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855	29	3.3	1458	9	BC011017	BC011017 Homo sapi	928	29	3.3	1771	9	BC014787	BC014787 Homo sapi
856	29	3.3	1459	9	AK026577	AK026577 Homo sapi	929	29	3.3	1774	5	BC045331	BC045331 Dantio rer
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858	29	3.3	1463	9	BC002572	BC002572 Homo sapi	931	29	3.3	1811	10	BC008612	BC008612 Mus muscu
859	29	3.3	1463	10	BC050896	BC050896 Mus muscu	932	29	3.3	1828	9	BC003610	BC003610 Homo sapi
860	29	3.3	1470	9	BC013436	BC013436 Homo sapi	933	29	3.3	1829	10	BC054468	BC054468 Mus muscu
861	29	3.3	1476	6	BD237281	BD237281 Secreted	934	29	3.3	1836	9	BC012136	BC012136 Homo sapi
862	29	3.3	1478	9	BC015888	BC015888 Homo sapi	935	29	3.3	1837	9	BC000716	BC000716 Homo sapi
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864	29	3.3	1494	9	AF070535	AF070535 Homo sapi	937	29	3.3	1839	6	AR404234	AR404234 Sequence
865	29	3.3	1507	6	AX354366	AX354366 Sequence	938	29	3.3	1839	6	BD223419	BD223419 94 human
866	29	3.3	1507	6	AX354369	AX354369 Sequence	939	29	3.3	1842	8	AY062110	AY062110 Arabidops
867	29	3.3	1507	6	BD082413	BD082413 87 human	940	29	3.3	1844	10	MUSNACHRC	M30514 Mouse muscl
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

QY 123 T 123
Db 121 T 121

RESULT 5

AX324676/c 121 bp DNA linear PAT 02-SEP-2002
LOCUS AX324676
DEFINITION Sequence 814 from Patent WO0192512.
ACCESSION AX324676
VERSION AX324676.1 GI:18095429
KEYWORDS
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1
AUTHORS Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
UNIVERSITY OF DELAWARE (US)
PATENT: WO 0192512-A 814 06-DEC-2001;
FEATURES
source Location/Qualifiers
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/db_xref="taxon:3750"

ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.1e-25;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGAGCGGGAGGTTGAGATCAAGAGATTGAGACTCAAGTACAGGAGGTGACCTA 62
Db 121 GGGAGCGGGAGGTTGAGATCAAGAGATTGAGACTCAAGTACAGGAGGTGACCTA 62
QY 63 CTCGAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGC 122
Db 61 CTCGAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGC 2
QY 123 T 123
Db 1 T 1

RESULT 6

AX324679 121 bp DNA linear PAT 02-SEP-2002
LOCUS AX324679
DEFINITION Sequence 817 from Patent WO0192512.
ACCESSION AX324679
VERSION AX324679.1 GI:18095432
KEYWORDS
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

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FEATURES
source Location/Qualifiers
1..121
/organism="Malus x domestica"
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/db_xref="taxon:3750"

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AUTHORS Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
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PATENT: WO 0192512-A 817 06-DEC-2001;
FEATURES
source Location/Qualifiers
1..121
/organism="Malus x domestica"
/mol_type="unassigned DNA"
/db_xref="taxon:3750"

ORIGIN

ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.1e-25;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGAGAGCTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACCTACTCC 66
Db 1 CGTGGAGAGCTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACCTACTCC 60
QY 67 AAGAGAGAAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGTAA 126
Db 61 TAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGTAA 120
QY 127 G 127
Db 121 G 121

RESULT 7
AX324680/c 121 bp DNA linear PAT 02-SEP-2002
LOCUS AX324680
DEFINITION Sequence 818 from Patent WO0192512.
ACCESSION AX324680
VERSION AX324680.1 GI:18095433
KEYWORDS
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1
AUTHORS Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
UNIVERSITY OF DELAWARE (US)
PATENT: WO 0192512-A 818 06-DEC-2001;
FEATURES
source Location/Qualifiers
1..121
/organism="Malus x domestica"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.1e-25;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGAGAGCTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACCTACTCC 66
Db 121 CGTGGAGAGCTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACCTACTCC 62
QY 67 AAGAGAGAAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGTAA 126
Db 61 TAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGTAA 2
QY 127 G 127
Db 1 G 1

RESULT 8

AX324683 121 bp DNA linear PAT 02-SEP-2002
LOCUS AX324683
DEFINITION Sequence 821 from Patent WO0192512.
ACCESSION AX324683
VERSION AX324683.1 GI:18095436
KEYWORDS
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1
AUTHORS Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
UNIVERSITY OF DELAWARE (US)
PATENT: WO 0192512-A 821 06-DEC-2001;
FEATURES
source Location/Qualifiers
1..121
/organism="Malus x domestica"
/mol_type="unassigned DNA"
/db_xref="taxon:3750"

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
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Matches 120;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;			
Query	28	AGGATTGAGAACTCAAGTAAACAGGAGGCTGACTCTACCAAGAGAGAAATGGGATTATC	87				
Db	1	AGGATTGAGAACTCAAGTAAACAGGAGGCTGACTCTACCAAGAGAGAAATGGGATTATC	60				
QY	88	AAGAAAGCAAAAGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATCT	147				
Db	61	TGAAGAGCAAAAGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATCT	120				
QY	148	A 148					
Db	121	A 121					
RESULT 9	AX324684/c	121 bp	DNA	linear	PAT 02-SEP-2002		
LOCUS	AX324684	Sequence 822 from Patent WO0192512.					
DEFINITION	AX324684						
ACCESSION	AX324684.1	GI:18095437					
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
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Matches 120;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;			
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Db	121	AGGATTGAGAACTCAAGTAAACAGGAGGCTGACTCTACCAAGAGAGAAATGGGATTATC	62				
QY	88	AAGAAAGCAAAAGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATCT	147				
Db	61	TGAAGAGCAAAAGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATCT	2				
QY	148	A 148					
Db	1	A 1					
RESULT 10	AX324687	121 bp	DNA	linear	PAT 02-SEP-2002		
LOCUS	AX324687						

	DEFINITION	Sequence 825 from Patent WO0192512.
	ACCESSION	AX324687
	VERSION	AX324687.1 GI:18095440
	KEYWORDS	
	SOURCE	Malus x domestica (apple tree)
	ORGANISM	Malus x domestica
	REFERENCE	Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J. Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 825 06-DEC-2001; UNIVERSITY OF DELAWARE (US) 1
	AUTHORS	Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
	TITLE	Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 825 06-DEC-2001; UNIVERSITY OF DELAWARE (US)
	JOURNAL	
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Dd	1 ATTGAGAACTCAAGTACAGCAGCGAGTGACTTCCACAAGAGAGAGATGTGATTATCAAG	60
Qy	AAGGAAGAAGCATCTACTCTTTATGTATGTATGTAAGTATCTCTTATCATTTATTCAGC	150
Dd	61 TAGGCAAAAGAGATCACTGTTCTATGTATGTATGTAAGTATCTCTTATCATTTATTCAGC	120
Qy	151 T 151	
Dd	121 T 121	
	RESULT 11	
	LOCUS	AX324688 121 bp DNA linear PAT 02-SEP-2002
	DEFINITION	Sequence 826 from Patent WO0192512.
	ACCESSION	AX324688
	VERSION	AX324688.1 GI:18095441
	KEYWORDS	
	SOURCE	Malus x domestica (apple tree)
	ORGANISM	Malus x domestica
	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus. 1 Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J. Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 826 06-DEC-2001; UNIVERSITY OF DELAWARE (US)
	AUTHORS	Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
	TITLE	Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 826 06-DEC-2001; UNIVERSITY OF DELAWARE (US)
	JOURNAL	
	FEATURES	location/Qualifiers 1..121 /organism="Malus x domestica" /mol_type="unassigned DNA" /db_xref="taxon:3750"
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	Query Match	8.1%; Score 70; DB 6; Length 121;
	Best Local Similarity	99.2%; Pred. No. 1.le-25;
	Matches	120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	ATTGAGAACTCAAGTACAGCAGCGAGTGACTTCCACAAGAGAGAGATGGATTATCAAG	90
Dd	121 ATTGAGAACTCAAGTACAGCAGCGAGTGACTTCCACAAGAGAGAGATGGATTATCAAG	62
Yy	AAGCAAAAGAGATCACTGTTCTATGTATGTATGTAAGTATCTTATCATTTATTCAGC	150

DEFINITION Homo sapiens hypothetical protein LOC339166, mRNA (cDNA clone
IMAGE:5163423), partial cds.
ACCESSION BC043508
VERSION BC043508.1 GI:27694155
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1929)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loguercio, N.A., Peters, G.J.,
Adrianson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Hellon, E., Kettelman, M., Madan, A., Rodighiero, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalim, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 12477932
FUEVED 2 (bases 1 to 1929)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
JOURNAL Submitted (09-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Boedet, Yaron Butterfield,
Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven
Ness, Pawan Pandon, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES
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Query March 3.9%; Score 34; DB 9; Length 1929;
Best local similarity 100.0%; Pred. No. 9.1e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1813 TTTGTGGGAAAAAAAAAAAAAAAAAAAAA 1846
RESULT 15
AF059273 1964 bp mRNA linear ROD 15-OCT-1998
LOCUS Rattus norvegicus glucocorticoid modulatory element binding protein
DEFINITION 2 mRNA, complete cds.
ACCESSION AF059273
VERSION AF059273.1 GI:3746540
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1964)
Zeng, H., Jackson, D.A., Oshima, H. and Simons, S.S. Jr.
Glucocorticoid modulatory element binding protein 2 (GMEB-2)
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1964)
Zeng, H., Jackson, D.A., Oshima, H. and Simons, S.S. Jr.
Direct Submission
JOURNAL Submitted (13-APR-1998) Steroid Hormones Sect., NIDDK/NIH, Bldg. 8,
Room B2A-07, Bethesda, MD 20892, USA
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/cell_line="Pus-5"
/tissue_type="liver"
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LDYFQDKVCSNTRCSTKXIDLSGARVLSPTSTEYIPLTPAADVNGSPAPITITETC
EDPDWTTTIGDPTFAFMWGLDAGLIDVIOEFOCELEETMKGLQORVQDPPLQIRD
AVLNNIVNFMGLDVKVYLASHKCOMDSREOVARDLALEQOCDEHRRRAKEIKH
KSOHLNNVMTLLPVLPLSPMKRPRRAATSGPAAAGVLTOSAGIALGPGMPMSOL
TSYPLKRVYSLPTSLTGKSGRQAAPASSPAPSLGGLTYVLASSGSGTPTSTYETHPDT
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GPEHRTATLEVAADHEOK"

Search completed: September 26, 2004, 01:07:34
Job time : 3746.18 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 15:45:02 ; Search time 2740.53 Seconds
(without alignments)

9458.147 Million cell updates/sec

Title: US-10-069-527-1
Perfect score: 868
Sequence: 1 atggagacgtcggaaggttga.....aaaaaaaaaaaaaaaaaaaaa 868

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	336.8	38.8	642	13	B0879372 V059D02 P

5	318.6	36.7	502	13	B0104186
6	312.4	36.0	503	13	B0106062
7	296.2	34.1	540	13	B0879741
8	295.8	34.1	488	13	B0104054
9	285.6	32.9	549	14	CB073377
10	280.4	32.3	585	13	B0857987
11	280.4	32.3	659	13	B0012873
12	279.4	32.2	637	13	B0013785
13	279.4	32.2	744	12	B1932285
14	279.4	32.2	751	12	B1932302
15	279.4	32.2	767	12	B1931714
16	279.4	32.2	771	12	B1932370
17	278.8	32.1	694	13	B0012106
18	278.8	32.1	706	13	B0991703
19	278.8	32.1	719	13	B0013737
20	278.8	32.1	736	13	B0013836
21	278.8	32.1	738	13	B0012321
22	276.4	31.8	534	12	BM528650
23	275.6	31.8	602	13	B0994818
24	275.6	31.8	698	13	B0994330
25	275.6	31.8	774	13	B0010787
26	275.6	31.7	686	13	B0851511
27	271.8	31.7	520	13	B0853867
28	270.4	31.2	745	14	CF373459
29	269.8	31.1	727	13	B0992097
30	268.4	30.9	646	14	CB971674
31	266.6	30.7	400	14	CF609891
32	266.4	30.7	492	13	B0105645
33	266.2	30.6	613	9	A1490968
34	265.6	30.6	537	10	BE807721
35	264	30.4	547	13	B0988714
36	263.8	30.4	551	10	AM922900
37	259.2	29.9	490	14	CB086405
38	257.8	28.7	436	10	BE805943
39	249.4	28.7	638	12	B0244728
40	242.6	27.9	643	12	B0246495
41	242.6	27.9	643	12	B0246495
42	242	27.9	814	9	AJ568642
43	241.6	27.8	642	12	B0248831
44	241.6	27.8	650	12	B0247197
45	240.8	27.7	607	10	BE493790

ALIGNMENTS

RESULT 1
LOCUS B1978968 719 bp mRNA linear EST 29-OCT-2002
DEFINITION zc06 Old Blush petal SMART library Rosa chinensis cDNA 5' similar
to MADS-box protein, mRNA sequence.

ACCESSION B1978968.1 GI:24420761
VERSION B1978968

KEYWORDS

SOURCE

ORGANISM

EST.

REFERENCE

AUTHORS

TITLE

ANALYSIS

Tags

FEBS Lett. 515 (1-3), 35-38 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Cock JM

RDP (UMR5667 INRA/CNRS/ENSL/UCBL)

Ecole Normale Supérieure de Lyon

46, Allée d'Italie, 69364 LYON Cedex 07, France

Tel: 33472728611

Db 273 GATGCAAAACATGAAATCTCAGCATGATTTGGATAGATCAAAAAGAGATGATAGC 332

Qy 301 ATGCAAGTAAAGCTCAGGCAATCTGAGAGAGAGATTAATCAATCATGTAAGCATGTGAG 360

Db 333 ATGCAAGTAAAGCTCAGGCAATCTGAGAGAGAGATTAATCAATCATGTAAGCATGTGAG 392

Qy 361 CTGATGAGCTTAAAG 420

Db 393 CTGATGAGCTTAAAG 452

Qy 421 AAGTTCGTGACATGATGAG 480

Db 453 GAATTTACAAAGATGCTCAAGAAAATCAAGAAATCTGAGAGAGAGAGAGAGAGAGAGAG 512

Qy 481 ACTTATGAGCTGCAAAAACAG 540

Db 513 AATTACATCGTGACCAACAG 572

Qy 541 AATGGTATCATCAG 600

Db 573 AGTGAATATCATCAG 623

Qy 601 GCCTTCGCGGTGACAGCTTATTCAGCCAAATCTCCAGAGAGAGATCTAATT 650

Db 624 GCCTTCGCGGTGACAGCTTATTCAGCCAAATCTCCAGAGAGAGATCTAATT 673

RESULT 3

LOCUS B1978971 723 bp mRNA linear EST 29-OCT-2002

DEFINITION ZC09.Old Blush petal SMART library Rosa chinensis cDNA 5' similar to MADS-box protein, mRNA sequence.

ACCESSION B1978971

VERSION B1978971.1 GI:24420763

KEYWORDS EST.

SOURCE Rosa chinensis

ORGANISM Rosa chinensis

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Rosales; Rosaceae; Rosoideae; Rosa.

AUTHORS 1 (bases 1 to 723)

Channeliere, S., Riviere, S., Scalliet, G., Szecsi, J., Jullien, F., Dolle, C., Vergne, P., Dumas, C., Bendahmane, M., Huguene, P. and Cock, J.M.

TITLE Analysis of gene expression in rose petals using expressed sequence tags

JOURNAL FEBS Lett. 515 (1-3), 35-38 (2002)

MEDLINE 21940574

PUBMED 11943190

COMMENT Contact: Cock JM

RDP (UMR5667 INRA/CNRS/ENSL/UCBL)

Ecole Normale Supérieure de Lyon

46, Allée d'Italie, 69364 LYON Cedex 07, France

Tel: 33472728611

Fax: 33472728600

Email: Mark.Cock@ens-lyon.fr

PCR Primers

FORWARD: CTGGGAAGCGCGCATTTGTGTGT

BACKWARD: ATACGACTCATATAGGCGCAATTTGGCC.

Location/Qualifiers

1..723

/organism="Rosa chinensis"

/mol_type="mRNA"

/strain="Botanical garden, Lyon"

/cultivar="Old Blush"

/db_xref="taxon:74649"

/sex="Hermaphrodite"

/dev_stage="Mixed (young bud, open bud, mature flower, senescing flower)"

/lab_host="Escherichia coli"

/clone_lib="Old Blush petal SMART library"

/note="Organ: Petal; Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI"

ORIGIN

Query Match 40.0%; Score 346.8; DB 12; Length 723;

Best Local Similarity 76.1%; Pred. No. 76-43;

Matches 497; Conservative 0; Mismatches 113; Indels 43; Gaps 4;

Qy 1 ATGGACGTGGAG 60

Db 83 ATGGAG 142

Qy 61 TACTCAAG 120

Db 143 TATTCTAAG 202

Qy 121 GCTAAGATATCTCTATATATTTATCTAGCTCTGGAGAGAGAGAGAGAGAGAGAGAG 177

Db 203 GCTAAGATATCTCTATATATTTATCTAGCTCTGGAGAGAGAGAGAGAGAGAGAGAG 262

Qy 178 CCTCAACTACGCTGACAGAAATCTT-AGACAAATATCATGACATCTGGAGAGAGAG 236

Db 263 CCTCAAG 322

Qy 237 GTGGAGATGTAAGCATGAGAACTTCAAGATGAGATGAGATGAGATGAGATGAGATGAG 296

Db 323 ATGGAGATGCAAGCATGAGAACTTCAAGATGAGATGAGATGAGATGAGATGAGATGAG 382

Qy 297 CAGCATGCAAGTAAAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356

Db 383 TGCGATGCAAAATGAGCTTGGCAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 442

Qy 357 AAGAGCTGATGCTTAAAG 416

Db 443 GGAAGCTGATGCTTAAAG 502

Qy 417 GTTCAAGTTCGTGACATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476

Db 503 GTTCAAGTTCGTGACATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562

Qy 477 CCTCACTTAAAGCTGCAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536

Db 563 CTTGCGATTCAGCTGACAAAT-ATGATGAAATATGAGAGAGAGAGAGAGAGAGAGAG 616

Qy 537 GGAAGATGCTATCATCAG 596

Db 617 G-----NACTACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 643

Qy 597 TTTTGGCTTCGCGGTGACAGCTTATTCAGCAATCTCCAGAGAGAGAGATCTAAT 649

Db 644 TTTTGGCTTCGCGGTGACAGCTTATTCAGCAATCTCCAGAGAGAGAGATCTAAT 696

RESULT 4

LOCUS BU879372 642 bp mRNA linear EST 16-OCT-2002

DEFINITION V059D02 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BU879372

VERSION BU879372.1 GI:24070896

KEYWORDS EST.

SOURCE Populus balsamifera subsp. trichocarpa

ORGANISM Populus balsamifera subsp. trichocarpa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Malpighiales; Salicaceae; Saliceae; Populus.

AUTHORS 1 (bases 1 to 642)

Umbarger, P., Bhalerao, R.R., Jansson, S. and Sterky, F.

The Poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

Unpublished (2002)

CONTACT: BHALRAO RUPALI R.

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Department of Plant Physiology

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 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.unu.se.
 Location/Qualifiers

FEATURES

1..642
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /tissue_type="floral buds"
 /clone_lib="Populus flower cDNA library"
 /note="Organ: flower"

ORIGIN

Query Match 38.8%; Score 336.8; DB 13; Length 642;
 Best Local Similarity 75.5%; Pred. No. 2,4e-41;
 Matches 432; Conservative 0; Mismatches 137; Indels 3; Gaps 1;

FEATURES

1..502
 /organism="Rosa hybrid cultivar"
 /mol_type="mRNA"
 /strain="Golden Gate"
 /db_xref="taxon:128735"
 /clone="g90294.e"
 /tissue_type="petals"
 /dev_stage="young open flower at stage four"
 /clone_lib="Rose Petals (Golden Gate) Lambda Zap Express Library"
 /note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

Query Match 36.7%; Score 318.6; DB 13; Length 502;
 Best Local Similarity 81.4%; Pred. No. 1.5e-38;
 Matches 382; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

ORIGIN

1 ATGGAGAGTGGAGAGTGGAGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 60
 74 ATGGAGAGTGGAGAGTGGAGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 133
 134 TACTCCAGAGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 120
 134 TACTCCAGAGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 193
 121 GCTAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 180
 194 GCTCAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 253
 181 TCAACTAGCTGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 240
 254 TCAACTAGCTGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 313
 241 GATGCTAGAGATGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 300
 314 GATGCTAGAGATGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 373
 301 ATCAAGTATGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 360
 374 ATCAAGTATGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 433
 361 CTGATGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 420
 434 TTATGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 493
 421 AAGTGGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 480
 494 GAGTGGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 553
 481 ACTTATGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 540
 554 CAGTGGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 610
 541 AATGGTATGATGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 572
 611 AATGGTATGATGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 642

RESULT 5
 BQ104186 502 bp mRNA linear EST 16-APR-2002
 LOCUS BQ104186
 DEFINITION g90294.e Rose Petals (Golden Gate) Lambda Zap Express Library Rosa
 hybrid cultivar cDNA clone g90294.e 5', mRNA sequence.
 ACCESSION BQ104186
 VERSION BQ104186.1 GI:20153848
 KEYWORDS EST.
 SOURCE Rosa hybrid cultivar
 ORGANISM Rosa hybrid cultivar
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
 Rosids; eustosids I; Rosales; Rosaceae; Rosoideae; Rosa.
 REFERENCE 1 (bases 1 to 502)

AUTHORS Guterman, I., Shalit, M., Menda, N., Pietersen, D., Dafny-Yelin, M.,
 Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J.,
 Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and
 Weis, D.
 TITLE Rose Scent: Genomics Approach to Discovering Novel Floral
 Fragrance-Related Genes
 JOURNAL Plant Cell 14 (10), 2325-2338 (2002)
 COMMENT Contact: Naama Menda
 Petal Genomics
 Faculty of Agricultural, Food and Environmental Quality Sciences,
 The Hebrew University of Jerusalem
 P.O. Box 12, Rehovot, 76100, Israel
 Tel: 972 8 9489 683
 Fax: 972 8 9468 265
 Email: shaham@agri.huji.ac.il
 Seq primer: T3 forward.
 Location/Qualifiers

FEATURES

1..502
 /organism="Rosa hybrid cultivar"
 /mol_type="mRNA"
 /strain="Golden Gate"
 /db_xref="taxon:128735"
 /clone="g90294.e"
 /tissue_type="petals"
 /dev_stage="young open flower at stage four"
 /clone_lib="Rose Petals (Golden Gate) Lambda Zap Express Library"
 /note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

Query Match 36.7%; Score 318.6; DB 13; Length 502;
 Best Local Similarity 81.4%; Pred. No. 1.5e-38;
 Matches 382; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

1 ATGGAGAGTGGAGAGTGGAGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 60
 34 ATGGAGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 93
 61 TACTCCAGAGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 120
 94 TACTCCAGAGAGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 153
 121 GCTAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 177
 154 GCTCAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 213
 178 CCTCAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 237
 214 CCTCAAGTATCTCTTCAATTTATTTAGCTCTGGAAGATGTTGAATCTGAGCCCT 273
 238 TGGATGCTAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 297
 274 TGGATGCTAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 333
 298 AGCATGGAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 357
 334 GGCATGGAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 393
 358 GAGCTGATGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 417
 394 GAGCTGATGAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 453
 418 TCCAGTCTGCTCAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 466
 454 TCCAGTCTGCTCAAGTGGAGAGTGGAGATTCAGAGAGAGAGATCACTGTTCTATGTGAT 502

RESULT 6
 BQ106062 503 bp mRNA linear EST 16-APR-2002
 LOCUS BQ106062
 DEFINITION fc1436.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
 Rosa hybrid cultivar cDNA clone fc1436.e 5', mRNA sequence.
 ACCESSION BQ106062

VERSION B0106062.1 GI:20155724
KEYWORDS EST.
SOURCE Rosa hybrid cultivar
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 503)
AUTHORS Guernan,I., Shalit,M., Menda,N., Plestun,D., Dafny-Yelin,M., Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J., Adam,Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and Weiss,D.
TITLE Rose Scent: Genomics Approach to Discovering Novel Floral Fragrance-Related Genes
JOURNAL Plant Cell 14 (10), 2325-2338 (2002)
COMMENT Contact: Naama Menda
Petal Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem
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Tel: 572 8 9489 683
Fax: 972 8 9468 265
Email: shaham@agri.huji.ac.il
Seq primer: T3 forward.
FEATURES
source 1..503
Location/Qualifiers
1..503
/organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc1436.e"
/tissue_type="Petal"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 36.0%; Score 312.4; DB 13; Length 503;
Best Local Similarity 82.4%; Pred. No. 1.3e-37;
Matches 371; Conservative 0; Mismatches 76; Indels 3; Gaps 1;
QY 1 ATGGACGTGGAGAGTTGAGATCAAGAGATTGAGAACTCACTAACAGGAGTACC 60
DB 51 ATGGGAGAGGGTAAGATTGATTAAGAGATTGAAACTCAAGCAACAGGAGTACC 110
QY 61 TACTCCAAAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTTATGTGAT 120
DB 111 TATCTTAAGAGAAAGATGGATCATCAAGAGGCTAAGAGAAATCACTGTTCTTGTGAT 170
QY 121 GCTAAGATCTCTTATCATTTATTTAGCTCTGGGAAAGTGTGAATCTGCA---GC 177
DB 171 GCTAAGTTTCTTATATATCATTTGCTGTAAGTCTGGAATAATGTTGAATCTGAGGCG 230
QY 178 CTTTCAACTACGCTGACAGAAATCTTGGACAAATACATGAGCAATTTGGAGAGATTG 237
DB 231 CCTCAGAGAAAGCGAGATGAAATCTTGGACAAATACATGAGCACTGAGAAAGAGTTA 290
QY 238 TGGAGTGTAGATGAGAGAACTCAGCAATGAGTGTAGAGTCAGAGAAAGCAATGAG 297
DB 291 TGGATGTCAGATGAGAGAACTCTGCAATGATGATAGAGTCAGAGAAAGCAATGAT 350
QY 298 AGCATGAGTAGAGCTCAGGCATCTGAAGGAGAGAGATATCATATTGAACCATGTA 357
DB 351 GGCATGCAAAATTGAGCTTCGGCATTTGAGGGGAGAGACATTAACATCTGAGACCATGTG 410
QY 358 GAGCGATAGGCGCTTAGAGAGAGCACTTGAAATGGCCTTCAATATCCGGAGCAACAG 417
DB 411 GACCTGATGCGCTTAGAGAGAGCAATTAATGCGCTTGCAGATATCAGAGCAATG 470
QY 418 TCCAGATTCTGCAATGATGAGAGACAT 447
DB 471 TCGAAGTACATGAGCGGCTTAGAGAAAT 500

RESULT 7
BU879741 540 bp mRNA linear EST 16-OCT-2002
LOCUS V063H01 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.
DEFINITION
ACCESSION BU879741 GI:24071265
VERSION BU879741
KEYWORDS EST.
SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE 1 (bases 1 to 540)
AUTHORS Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
JOURNAL Unpublished (2002)
COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
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Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
FEATURES
source 1..540
Location/Qualifiers
1..540
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"

ORIGIN
Query Match 34.1%; Score 296.2; DB 13; Length 540;
Best Local Similarity 78.4%; Pred. No. 3.3e-35;
Matches 355; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 ATGGACGTGGAGAGTTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGTACC 60
DB 87 ATGGGAGAGGTAAGATTGATTAAGAGATTGAAACTCAAGCAACAGGAGTACC 146
QY 61 TACTCCAAAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTTATGTGAT 120
DB 147 TACTCCAAAGAGAGAGATGGATCATTAAGAGAGAGAGATCACTGTTTATGTGAT 206
QY 121 GCTAAGATCTCTTATCATTTATTTAGCTCTGGGAAAGTGTGAATCTGAGAGCCT 180
DB 207 GCTCAAGTTTCTTGTCTCATCTTTGCTAGTTCTGAGAGATCAAGAGTCTGAGCCT 266
QY 181 TCACTAGCGTGAAGAAATCTTGGACAAATACATGAGCAATCTGGAGAGAGTTGTG 240
DB 267 TCCACTACCGTGTGATGATGTTGAGCAAGTATCAAGCAATCTGTAAGAGCGTGTG 326
QY 241 GATGCTAACATGAGAGAACTCAGCAATGAGTGTAGAGTCAGAGAAAGCAATGAGC 300
DB 327 GATGCTAACATGAGAGAACTCAGCAACGAGATTGACAGATTAAGAGAAAGCAATGAGC 386
QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGATATCATATTGAACCATGTAAG 360
DB 387 ATGCAATATGAGAGCTGAGGCATCTGAAGGAGAGATATCATCTTTGGCCCAAAAGG 446
QY 361 CTGATGCGCTTAGAGAGCACTTGAATAATGGCCTTACAAGTATCCGGAGCAAGAGTCC 420
DB 447 TTGATGCGCATGAGAGAGCCCTTGAATATGAGCCTTGTGCTGCTCGTAAAGAGAGATG 506
QY 421 AAGTTCGTGACATGATGAGAGCAATGGAAG 453
DB 507 GAGTTCACAGCATGTTGAGCAAAATGAAAG 539

RESULT 8
LOCUS B0104054 488 bp mRNA linear EST 16-APR-2002
DEFINITION B0104054 Rose Petals (Fragrant Cloud) Lambda Zap Express Library
ACCESSION B0104054 Rose hybrid cultivar cDNA clone fc2302.e 5', mRNA sequence.
VERSION B0104054.1 GI:20153716
KEYWORDS EST.
SOURCE Rosa hybrid cultivar
ORGANISM Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
1 (bases 1 to 488)
Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M.,
Shalev, G., Bar, E., Dayadov, O., Ovadis, M., Emanuel, M., Wang, J.,
Adam, Z., Pichersky, E., Lewinson, E., Zamir, D., Vainstein, A. and
Weiss, D.
Rose Scent: Genomics Approach to Discovering Novel Floral
Fragrance-Related Genes
Plant Cell 14 (10), 2325-2338 (2002)
Contact: Naama Menda
Petat Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel
Tel: 972 8 9489 683
Fax: 972 8 9468 265
Email: shahamagri.huji.ac.il
Seq primer: T3 forward
Location/Qualifiers
1..488
/organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc2302.e"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/note="Vector: pBKCW; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 34.1%; Score 295.8; DB 13; Length 488;
Best Local Similarity 79.0%; Pred. No. 4e-35;
Matches 380; Conservative 0; Mismatches 92; Indels 9; Gaps 2;
Db 62 ACTCCAGAGAGAGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGATG 121
|||
3 ACCGAGAGAGAGAGATGGATCATCAAGAGCTTAAGAGAACTGTTCTTGTGATG 62
|||
122 CTAAAGTATCTTTATCATTTATTTAGCTCTGGGAAAGTGTGAATCTGCA--GCC 178
|||
63 CTAAAGTCTCTTATATCATTTAGCTCTGAAAAAATGTTGAATCTGAGCGGCC 122
|||
179 CTTCACATAGCGCGAGCAAAATCTTGACAAATATACATGGAGCAATCGGAGAAAGTGT 238
|||
123 CTACGAGAAACGCGAGTAAATCTTGACAAATATCACTCAAGTCTGAAAAAGTTAT 182
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239 GGGATGCTTAAGCATGAGAACCTTGCATGATGATGATGATGATGATGATGATGATG 298
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183 GGGATGCTTAAGCATGAGAACCTTGCATGATGATGATGATGATGATGATGATGATG 242
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299 GCATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 358
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243 GCATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 302
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359 AGCTGATGCTTATGAGAGAGCACTTGAATGAGCTTCAAGTATCCGAGCAAGACAT 418
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303 ACCTGATGCTTATGAGAGAGCACTTGAATGAGCTTCAAGTATCCGAGCAAGACAT 362
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RESULT 9
LOCUS CB077377 549 bp mRNA linear EST 24-JAN-2003
DEFINITION CB077377 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
terminalis cDNA clone h53a08, mRNA sequence.
ACCESSION CB077377 GI:27890814
VERSION CB077377.1
KEYWORDS EST.
SOURCE Hedyotis terminalis
ORGANISM Hedyotis terminalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
Spermacoceae; Hedyotis.
1 (bases 1 to 549)
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balis, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis terminalis flower - Stage 2
(NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lila Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: h53 row: a column: 08
Seq primer: -21M13UnivRev
High quality sequence stop: 549.
Location/Qualifiers
1..549
/organism="Hedyotis terminalis"
/mol_type="mRNA"
/db_xref="taxon:219667"
/clone="h53a08"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: StrataGene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN
Query Match 32.9%; Score 285.6; DB 14; Length 549;
Best Local Similarity 71.6%; Pred. No. 1.3e-33;
Matches 375; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
Db 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGTGACC 60
|||
26 ATGGGAGAGTAAAGATTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGTGACT 85
|||
61 TACTCCAGAGAGAGAAATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGAT 120
|||
86 TACTCCAGAGAGAACTGGGATCATGAAAAAGCTTAGAGAAATCACTGTTCTTGTGAT 145
|||

QY	121	GCCTAAGATCTCTTATCATTTATCTAGCTCTGGGAAGATGGTGAATACGACGCGCT	180
Db	146	GCTAAGATTCCTTATCATCTCCGATCTCTGGGAAGATGCATGATTAATCATCACTGCTCT	205
QY	181	TCAACTACGCTGACGAATACTTTGGACAAATTCATGACAAATCTGGGAGAGATGTGGTG	240
Db	206	TCAACTAATTTGGTTCATATGCTGGATGCTTACCAAGATCTACCTGGAGAGAACTATGG	265
QY	241	GATGCTAGCATGAGAAACCTGAGCAATGAGTGAATAGTCACAAAGAACAAATGACACG	300
Db	266	GATTTTAAGCATGAGAGTTTAAAGCATGAAATCGATCGATCAAGAAAGAGATACACAC	325
QY	301	ATGCAGTAGAGCTCAGGCATCTGAAGGAGAGAGATATCACTCATTTAAACCATGTAGAG	360
Db	326	ATGCAGATTTAACTGAGGCACTGAAAGGAGACGATATCTCAAAATTTGAATCTACAAAGAA	385
QY	361	CTGATGCGCTTAGAGAGAACCTTGAAATGCGCTTACAAAGTATCGGGACAAAGCATGCC	420
Db	386	CTGATGCGCTTAGAGATTCACCTTGAAATGCGCTTATCGGTTTACTGACCAACAGAGT	445
QY	421	AAGTTCTGCGACATGATGAGAGCAATGGAAGGACCTGGAAAGATGAATTAAGGCGCTC	480
Db	446	GAGATTCCTCAAGATGATGAGGAAATATGATCAAAATGTTGGAGAGAGAGCTCAAGCAGCTT	505
QY	481	ACTTATGAGCTGCAGAAAACAACAGAGATGAAATTAAGAGAGA	524
Db	506	CAGTTCATGTTGCATCGACGAGATATGGCCAGCATGAAAGGAAA	543

ORIGIN

incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpbd.ucdavis.edu>. TAG_LIB=Q5_AECID lettuce salinas TAG_SEQ=CGATGCGG3"

Query Match	32.3%;	Score 280.4;	DB 13;	Length 559;
Best Local Similarity	72.7%;	Pred. No. 7.5e-33;		
Matches 362;	Conservative 0;	Mismatches 136;	Indels 0;	Gaps 0

RESULT	10
LOCUS	BQ857987
DEFINITION	BQ857987 559 bp mRNA linear EST 14-AUG-2002
ACCESSION	CG99A17.YE.ab1 CG_IACDI lettuce salinas Lactuca sativa cDNA clone
VERSION	BQ857987
KEYWORDS	BQ857987.1 GI:22243452
SOURCE	EST.
ORGANISM	Lactuca sativa Lactuca sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca. 1 (bases 1 to 559) Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., Van Damme,M., Lavelle,D., Chevalier,P., Ziegler,T., Ellison,P., Kolman,J., Stalbaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
AUTHORS	
TITLE	

Oy	1	ATGGGACGTGGGAAAGGTTGAGATCAAGGAGTTGAGAACTCAAGTAAACGGCAGGTGAC	60
Db	23	ATGGGAGAGGAAATATAGATCAAGGAGTAGAGAAACCTGAGCAACGACAGTCAAC	82
Oy	61	TACTCCAAAGGAGGAAATGGATTATCAAGAGCCAAAGGATCACTGTTCTATGTAT	120
Db	83	TACTCCAAAGGAGGAAATGGAAATCATCAAGAAAGCTAAAGAAATCACTGTTCTGTGAT	142
Oy	121	GCTAAAGTATCTCTATCATTTATTTAGCTCTGGAGAGATGGTGAATATCTGCAGCCCT	180
Db	143	GCTAAAGTCTCTCTGTTATCTGTGGCTCTTGAGAAAGATGTATGAAATCTGTACCCC	202
Oy	181	TCACTAGCGTGACGAAATCTTGACCAATACCATGACCAATCTGGGAAAGATTGTGG	240
Db	203	AAAACCAATTGATGACATCTGGATCGAATGCAATGAAAGGCTTCTGGAAATAGGTTGTGG	262
Oy	241	GATGTAAACATGAGAAACCTCAGCAATGATGATGAGTCAAGAAAGCAATGACAC	300
Db	263	GATGCAAAACATGAGAAATCTGCAGATGAAATTTGATGATCAAGAAAGGAAACGAAAC	322
Oy	301	ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCAATCATTTGAACCATGTAGAG	360
Db	323	ATGCAAAATGAGACTCAGGCACCTTAAAGGGGAAAGATTAACATCGTTGAACATATGAAGAG	382
Oy	361	CTGATGAGCTTAGAGGAAGCACTTGAAAAATGGCTTCAAGTATCCGGGCAAGCAGCTGC	420
Db	383	CTAATTGCGTATGAAAGATGACACTTGAAGACGAACTCCAAACATCTGTGAGAAAGGAT	442
Oy	421	AAGTTGTCGACATGATAGAGACATAGAAAGGCACTGGAAGATGGAATTAAGCGCTTC	480
Db	443	GAAATCCCTAAATATCATAGGAAAGCATGAAACAAAGTACTGAGGAAGGAAATAGCATCTA	502
Oy	481	ACTTATGAGCTGCAAAA 498	
Db	503	ATGTATCTTGTGCACAA 520	

JOURNAL COMMENT
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michmore]
Department of Vegetable Crops, R.W.Michmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michmore@vegmail.ucdavis.edu]
belongs to contig QC_Ca_Contig7827, see <http://cgpdb.ucdavis.edu/>
for details.
Plate: QG59. row: A column: 17.
Location/Qualifiers
1. 559

RESULT 11			
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DEFINITION	BU012873	685 bp	MRNA linear EST 22-AUG-2001
ACCESSION	CGJ3C04.Y9.ab1	OG EFGH	lettuce serriola
VERSION	CGJ3C04	mnna	sequence.
KEYWORDS	BU012873		
SOURCE	BU012873.1	GI:22447268	
ORGANISM	Lactuca sativa		
	Lactuca sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		

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cultivar="Salinas"
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clone="QGS9A17"
lab_host="E. coli"
clone_1fb="QGABCDI lettuce salinas"
note="Vector: pBRCDMS11b; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that

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JOURNAL
COMMENT

Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
Belongs to contig QG_Ca_contig7827, see <http://cgdb.ucdavis.edu/>
for details.
Plate: QGJ3 row: C column: 04.

FEATURES

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/lab_host="E.coli"
/note="Vector: DBRCNDSFIAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG_SEQ=Not found"

ORIGIN

Query Match 32.3%; Score 280.4; DB 13; Length 685;
Best Local Similarity 72.7%; Pred. No. 6.6e-33;
Matches 362; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
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QY 61 TACTCCAGAGAGAGAGATGAGATTCAGAGAGAGAGAGTCACTGTTCTATGTAT 120
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QY 121 GCTAAGTATCTTATCATTTATTTAGCTCTGGAGAGATGTTGATTAAGTCAAGCCCT 180
DB 122 GCTAATGCTCTCTTGTATCTGTGCTCTTCTGGAGAGATGATTAAGTCAAGCCCT 181
QY 181 TCAACTACGCTGACAGAAATCTTGAACAATACCATGACCAATCTGGAGAGATGTTG 240
DB 182 AAATCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
QY 241 GATGCTAAGATGAGAACTCAGCAATGAAAGTGAAGTGAAGTCAAGAGAGATGACAGC 300
DB 242 GATGCAAAACATGAGAAATCTGCAAAATGAAATGATAGATCAAGAGAGAGAGAGC 301
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QY 361 CTGATGCTTGAAGAGAGATTCGAAATGAGCTTACAAATATCCGGAGACAGCAGCTCC 420
DB 362 CTATATGCTGATGAGATGAGATTCGAAATGAGCTTACAAATATCCGGAGAGAT 421
QY 421 AAGTTCGATGATGATGAGAGATTCGAAATGAGCTTACAAATATCCGGAGAGAT 480
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QY 481 ACTTATGAGCTGAGAGAG 498
DB 482 ATGATATCTTGTGACAGAA 499

RESULT 12

LOCUS BU013785 637 bp mRNA linear EST 22-AUG-2002
DEFINITION QGJ5J13.YG.ab1 QG_EFGHJ lettuce serricola Lactuca sativa cDNA clone QGJ5J13, mRNA sequence.
ACCESSION BU013785
VERSION BU013785
KEYWORDS BU013785.1 GI:22448180
SOURCE EST
ORGANISM Lactuca sativa

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
Belongs to contig QG_Ca_contig7827, see <http://cgdb.ucdavis.edu/>
for details.
Plate: QGJ5 row: J column: 13.

FEATURES

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/db_xref="taxon:4236"
/clone="QGJ5J13"
/lab_host="E.coli"
/note="Vector: DBRCNDSFIAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG_Lib=QG_EFGHJ lettuce serricola
TAG_SEQ=GCTTGAAGGG"

ORIGIN

Query Match 32.2%; Score 279.4; DB 13; Length 637;
Best Local Similarity 72.5%; Pred. No. 9.9e-33;
Matches 361; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
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DB 9 ATGGGAGAGAGAGATGAGATCAAGAGATGAGAACCTAGCAACAGACAGTACCC 68
QY 61 TACTCCAGAGAGAGAGATGAGATTCAGAGAGAGAGAGTCACTGTTCTATGTAT 120
DB 62 TACTCAAGAGAGAGATGAGATTCAGAGAGAGAGAGTCACTGTTCTATGTAT 128
QY 121 GCTAAGTATCTTATCATTTATTTAGCTCTGGAGAGATGTTGATTAAGTCAAGCCCT 180
DB 122 GCTAATGCTCTCTTGTATCTGTGCTCTTCTGGAGAGATGATTAAGTCAAGCCCT 181
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Db 189 AAAACCACTGATTGACATCTGATGATATCAAAAGCTTCTGGAATTAAGTTGTGG 248
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 Db 249 GATGCAAAACATGAGATCTGACAGATGAATTAATGATGATCAAGAAAGAAAGCAAGC 308
 QY 301 ATGCAAGTAGAGCTCAGGACATCTGAGAGAGAGATATCATCTATTGAAACCATGTGAG 360
 Db 309 ATGGAATATGAGCTCAGGACCTTAAAGGGGMAATTAACATCTGTTGAATGAGAG 368
 QY 361 CTGATGCGCTTAAAGAGACCTTGAATAATGCGCTTCAAGTATCCGAGCAAGACATCC 420
 Db 369 CTATTTGCGATGAGATGACCTTGAATAATGATCTCAACCATCTGTTGAGAAAGAT 428
 QY 421 AAGTTCTGACATGATGAGACATGAAAGGACATGAAAGATGAAATTAAGCGCTC 480
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 Db 489 ATGTACTTGTGCACAAA 506

RESULT 13

BI932285 744 bp mRNA linear EST 18-OCT-2001
 LOCUS EST552174 tomato flower, 8 mm to preanthesis buds Lycopersicon
 DEFINITION esculentum cDNA clone CTC22L11 5' end, mRNA sequence.

ACCESSION BI932285
 VERSION BI932285.1 GI:16246757
 KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 744)
 van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
 Uteback, T., Van Aken, S., Roming, C.M., Niemman, W., Fraser, C.M.,
 Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
 Generation of ESTs from tomato flower tissue, buds 8 mm -
 preanthesis

TITLE Unpublished (2001)
 JOURNAL Contact: CUGI
 COMMENT Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute

FEATURES
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 Location/Qualifiers
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 /tissue_type="flower"
 /dew_stage="buds 8mm to preanthesis"
 /clone_lib="tomato flower, 8 mm to preanthesis buds"
 /note="(Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
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 Institute for Genomic Research; flower buds and flowers
 were taken from greenhouse plants (4-8 wks old, TA496).
 They were immediately frozen in liquid nitrogen and then
 size-separated while remaining frozen."

ORIGIN

Query Match 32.2%; Score 279.4; DB 12; Length 744;
 Best Local Similarity 66.2%; Pred. No. 8.9e-33;
 Matches 419; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

QY 31 ATTGAGACTCAAGTACAGGAGGTGACTTACTCCAAAGAGAGGAATGGATTATCAAG 90
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 Db 61 AAGCTTAAGAAATTAATCTGTTTCTTTGAGCTAAGTTTCTCTTAATATCTTCTAGT 120
 QY 151 TCTGGAGAGATGTTGAATATCTGAGCCCTTCACTAGCTGACAGAAATCTTGACAAA 210
 Db 121 TCTGGAGAGATGATGATATTTGAGCCCTTCTACTAGATGATGATATGTTGATGGT 180
 QY 211 TACCATGACATCTTGGAGAGAGTGTGGATGTTAAGCATGAGAACTTCAGCATGAA 270
 Db 181 TATCAAAAAGCTTCTGGAGAGAGTGTGGATGTTAAGCATGAGAAATTTGATGATA 240
 QY 271 GTGATAGAGTCAAGAAAGACATGACAGATGACAGTATGAGCTGAGCATCTGAAGGA 330
 Db 241 ATTGATGATCAAGAAAGAGATGACATGATGAGCTTAAAGCTGAGGCACTCAAGGA 300
 QY 331 GAGATATCAATCATTTGAAACCATGATGAGCTGATGAGCCCTTGAAGAGACATTTAAAT 390
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 QY 571 TACAACACACACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 630
 Db 538 GAAGGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 QY 631 CTCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
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RESULT 14

BI932302 751 bp mRNA linear EST 18-OCT-2001
 LOCUS EST552191 tomato flower, 8 mm to preanthesis buds Lycopersicon
 DEFINITION esculentum cDNA clone CTC22N23 5' end, mRNA sequence.

ACCESSION BI932302
 VERSION BI932302.1 GI:16246774
 KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 751)
 van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
 Uteback, T., Van Aken, S., Roming, C.M., Niemman, W., Fraser, C.M.,
 Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
 Generation of ESTs from tomato flower tissue, buds 8 mm -
 preanthesis

TITLE Unpublished (2001)
 JOURNAL Contact: CUGI
 COMMENT Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute

Query Match 32.2%; Score 279.4; DB 12; Length 744;
 Best Local Similarity 66.2%; Pred. No. 8.9e-33;
 Matches 419; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
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FEATURES

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/dev_stage="buds 8mm to preanthesis"
/clone_id="tomato flower, 8 mm to preanthesis buds"
/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Query Match 32.2%; Score 279.4; DB 12; Length 751;
Best Local Similarity 66.2%; Pred. No. 8.8e-33;
Matches 419; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

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QY 31 ATTGAGAACTCAAGTAAAGGAGGAGTGAAGTCAAGAGGAGGAGTATTCAG 90
DB 1 ATGAAAACAAACAAAGGAGGAGTGAAGTCAAGAGGAGGAGTATTCAG 60
QY 91 AAGGCAAGGAGTCACTGTTCTATGATGATGATGATGATGATGATGATGAT 150
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QY 151 TCTGGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
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DB 478 GAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 537
QY 571 TACAACAAACAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 630
DB 538 GAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 597
QY 631 CTCAGAGAGATCTAATAGATATATCTTGC 663
DB 598 CTCAGAGAGATCTAATAGATATATCTTGC 630

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LOCUS BI931714
DEFINITION EST551603 tomato flower, 8 mm to preanthesis buds Lycopersicon
esculentum cDNA clone CTC20J20 5' end, mRNA sequence.
ACCESSION BI931714

VERSION BI931714.1 GI:16246186
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 767)
van der Hoeven R.S., Bezzerides J.L., Karmyheva S.A., Tsai J.,
Utterback T., Van Aken S., Rönning C.M., Niemann W., Fraser C.M.,
Martin G.B., Giovannoni U.J. and Tanksley S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
preanthesis
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.

FEATURES

source

Location/Qualifiers
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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/db_xref="taxon:4081"
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/tissue_type="flower"
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/clone_id="tomato flower, 8 mm to preanthesis buds"
/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Query Match 32.2%; Score 279.4; DB 12; Length 767;
Best Local Similarity 66.2%; Pred. No. 8.7e-33;
Matches 419; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

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QY 31 ATTGAGAACTCAAGTAAAGGAGGAGTGAAGTCAAGAGGAGGAGTATTCAG 90
DB 1 ATGAAAACAAACAAAGGAGGAGTGAAGTCAAGAGGAGGAGTATTCAG 60
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QY 151 TCTGGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
DB 121 TCTGGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 211 TACCATGACATCTGGAAGAGAGTGGAGTGAAGTGAAGTGAAGTGAAGTGA 270
DB 181 TATCAAAAAGCTTCTGGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
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QY 331 GAGGATGACATGATGACATGATGACATGATGACATGATGACATGATGACAT 390
DB 301 GAGGATGACATGATGACATGATGACATGATGACATGATGACATGATGACAT 360
QY 391 GGCCTTCAAGATCCGGAGCAAGAGTCCAGTCCAGTCCAGTCCAGTCCAGT 450
DB 361 GGCCTTCAAGATCCGGAGCAAGAGTCCAGTCCAGTCCAGTCCAGTCCAGT 420
QY 451 AAGGCAAGGAGTCACTGTTCTATGATGATGATGATGATGATGATGATGAT 510

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Db 421 CAAATTCTGGAGGAGGAAAAATPAAGCACTTCAATATGCTTTGC--ACCAAAAGAGATG 477
 QY 511 AAAATTAAGAGATGTGAGAAACATGGAATAATGGTATCATCAGAGGCACTGGGGAAC 570
 Db 478 GGAGCCATTGTGTGAGAGTGAAATATGAGAGAAATTCATGAGAGTGTATCATCAAGA 537
 QY 571 TACAACAACACACGACGACGATACCTTTGGCTTCCGCGTGACGCTTATTCAGCCAAT 630
 Db 538 GAAAGGATTATGAGTACCAATGCAATTTGGCTTACAGGTGACCAATGACCAAT 597
 QY 631 CTCAGGAGAGATCTAATTAGATATATCTTGC 663
 Db 598 CTACATGAAAGATGTAAATTTATTTAATTC 630

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Mon Sep 27 09:56:00 2004

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Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 16:09:57 / Search time 476.696 Seconds
(without alignments)
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Gapop 10.0, Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	308.2	35.5	900	US-10-425-114-10295	Sequence 10295, A
3	308.2	35.5	933	US-10-424-599-32218	Sequence 32218, A
4	307	35.4	535	US-09-732-627A-3282	Sequence 3282, A
5	303.2	34.9	649	US-10-021-323-8689	Sequence 8689, Ap
6	302.2	34.8	1007	US-10-425-114-14870	Sequence 14870, A
7	302.2	34.8	1021	US-10-424-599-65326	Sequence 65326, A
8	301.2	34.7	474	US-09-732-627A-4667	Sequence 4667, Ap
9	296.6	34.2	601	US-10-021-323-13542	Sequence 13542, A
10	296.6	34.2	639	US-10-021-323-13542	Sequence 8682, Ap
11	265.2	30.6	896	US-10-278-536-238	Sequence 238, App
12	265.2	30.6	914	US-10-412-699B-55	Sequence 55, Appl
13	233.6	26.9	1148	US-10-425-114-26809	Sequence 26809, A
14	217.8	23.1	3265	US-10-437-563-9922	Sequence 9922, Ap

15	216.8	25.0	657	13	US-10-425-114-4580	Sequence 4580, Ap
16	215.2	24.8	779	13	US-10-425-114-12120	Sequence 12120, A
17	188.8	21.8	306	12	US-09-732-627A-3518	Sequence 3518, Ap
18	187.2	21.6	310	12	US-09-732-627A-3967	Sequence 3967, Ap
19	175	20.2	1242	16	US-10-260-238-499	Sequence 499, App
20	154.4	17.8	1536	13	US-10-425-114-23106	Sequence 23106, A
21	148.4	17.1	1536	13	US-10-425-114-21316	Sequence 21316, A
22	148.2	17.1	681	15	US-10-104-580-3	Sequence 3, Appl1
23	148.2	17.1	946	15	US-10-104-580-2	Sequence 2, Appl1
24	141	16.2	1036	13	US-10-424-599-120794	Sequence 120794, A
25	140.6	16.2	2718	13	US-10-424-599-120795	Sequence 120795, A
26	138.4	15.9	390	12	US-09-922-293-1337	Sequence 3337, Ap
27	138.2	15.9	871	13	US-10-425-114-10670	Sequence 10670, A
28	136.8	15.8	498	12	US-09-732-627A-4479	Sequence 4479, Ap
29	136.8	15.8	644	17	US-10-021-323-8631	Sequence 8631, Ap
30	136.6	15.7	407	12	US-09-922-293-3294	Sequence 3294, Ap
31	133.6	15.4	320	12	US-09-922-293-1	Sequence 1, Appl1
32	130.4	15.0	681	16	US-10-260-238-5530	Sequence 5530, Ap
33	130	15.0	2237	13	US-10-425-114-13120	Sequence 13190, A
34	129	14.9	258	12	US-09-922-293-1947	Sequence 1947, Ap
35	127	14.6	348	12	US-09-922-293-1197	Sequence 1197, Ap
36	127	14.6	730	17	US-10-767-701-7879	Sequence 7879, Ap
37	122.6	14.1	1212	13	US-10-425-114-11957	Sequence 11957, A
38	122.6	14.1	1231	13	US-10-425-114-15025	Sequence 15025, A
39	120.4	13.9	266	12	US-09-922-293-1948	Sequence 1948, Ap
40	120.2	13.8	1050	13	US-10-425-114-12758	Sequence 12758, A
41	120.2	13.8	1155	13	US-10-424-599-56649	Sequence 56649, A
42	119.6	13.8	425	12	US-09-922-293-14	Sequence 14, Appl
43	119.4	13.8	121	16	US-10-307-005-813	Sequence 813, App
44	119.4	13.8	121	16	US-10-307-005-814	Sequence 814, App
45	119.4	13.8	121	16	US-10-307-005-817	Sequence 817, App

ALIGNMENTS

RESULT 1
US-10-767-795-2121
; Sequence 2121, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yuhua
; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 2121
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C37363_1
US-10-767-795-2121

Query Match	37.9%	Score 329.4	DB 17	Length 951
Best Local Similarity	72.6%	Pred. No. 2.7e+83		
Matches 474	Conservative 0	Mismatches 161	Indels 18	Gaps 3
QY	1	ATGGAGCTGGAGAGTTGAGATCAAGAGATTGAGAACTCAAGTAACGAGGAGTGACC	60	
DB	41	ATGGGAGAGGCGAAGATTGAGATCAAGAGATTGAGAACTCAAGTAACGAGGAGTGACT	100	
QY	61	TACTCCAAAGGAGGAATGAGATTTCAGAGAGCAAGAGATCACTGTATGTGAT	120	
DB	101	TACTCAAAAGGAGGAATGAGATTTCAGAGAGCAAGAGATCACTGTATGTGAT	160	
QY	121	GCTAAGATCTCTTATCAATTTATTTAGCTCTGGAGAGATGATGATTAATCTGACCCCT	180	
DB	161	GCTAAGTTCTCTTATCAATCTTTGCTAGTTCTGGAGAGATGATGATTAATCTGACCCCT	220	

QY 181 TCACTACGCTGACAGAAATCTTGGACAAATACCATGACATCTGGAGAAAGTTGTG 240
Db 221 TCTACTAGTTGATGATGATTTTGGACCAATATCAGAAAATCTTGGGAAAAAGTTATGG 280
QY 241 GATGCTAAGATGAGAACTCTCAGCAATGAAAGTGATGAGTCAAGAAAGCAATGACAC 300
Db 281 GATGCTAAGATGAGAACTCTCAGCAATGAAAGTGATGAGTCAAGAAAGCAATGATAC 340
QY 301 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTTGAACCATGTAAG 360
Db 341 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTTGAACCATGTAAG 400
QY 361 CTGATGCTTGAAGAGAAAGCACTTGAATAATGCTTACAAATTCGCGGACCAAGCATCC 420
Db 401 CTGATGCTTGAAGAGAAAGCACTTGAATAATGCTTACAAATTCGCGGACCAAGCATCC 460
QY 421 AAGTTGCTGACATGATGAGAGACATGAGAAAGCACTGAGAGATGAGATTAAGGCCCTC 480
Db 461 GATGCTTATATGATGAGAGAAATATCCAAATTCCTGAGAGAGACATCAAGGACGCTC 520
QY 481 ACTATGAGCTGCAAAAACAAGAGATGAAATGAAAGATGTAAGAAACATGAGAA 540
Db 521 AGTTTCATCTGATCAACACACA--AGTGGCTTATGAAAGTGCAAGAGAG--CAGATGAT 577
QY 541 AATGGGATATGATGAGAGAGCTGGGGAACTACAAACAACCAAGAGAGATACCTTT 600
Db 578 CATGATACCCAGGAGACCCG-----GACTTACCACTCAGAGATGCTTCC 622
QY 601 GCCTTCGCTGAGGCTTATTCAGCCAAATCTCCAGAGAGAGATCTATTAGA 653
Db 623 ACCTTCAGTGAAGCAATGACGCCAACTTACAGAGAGAGATGTAATGA 675

RESULT 2
US-10-425-114-10295 ; Sequence 10295, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 10295
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700903463_FLI
US-10-425-114-10295

Query Match 35.5%; Score 308.2; DB 13; Length 900;
Best Local Similarity 75.6%; Pred. No. 3.1e-77;
Matches 382; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 1 ATGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACC 60
Db 74 ATGGAGGAGGGTAAAGATTGATCAAAAGATTGAGAACTCAAGCAACGGAAGTTACC 133
QY 61 TATCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGAGATCACTGTTCTATGTAT 120
Db 134 TATCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGAGATTAATGTTCTATGTAT 193
QY 121 GCTAAAGTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 180

Db 194 GCTCAAGTTCCCTTATCATCTTGTGTCCTGGAAGATGATGATCATCAGCCCC 253
QY 181 TCACTACGCTGACAGAAATCTTGGACAAATACCATGACATCTGGAGAAAGTTGTG 240
Db 254 TCACTAGTTGATGATGATGATTTTGGACCAATATCAGAAAATCTTGGGAAAAAGTTATGG 313
QY 241 GATGCTAAGATGAGAACTCTCAGCAATGAAAGTGATGAGTCAAGAAAGCAATGACAC 300
Db 314 GATGCTAAGATGAGAACTCTCAGCAATGAAAGTGATGAGTCAAGAAAGCAATGATAC 373
QY 301 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTTGAACCATGTAAG 360
Db 374 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTTGAACCATGTAAG 433
QY 361 CTGATGCTTGAAGAGAAAGCACTTGAATAATGCTTACAAATTCGCGGACCAAGCATCC 420
Db 434 CTGATGCTTGAAGAGAAAGCACTTGAATAATGCTTACAAATTCGCGGACCAAGCATCC 493
QY 421 AAGTTGCTGACATGATGAGAGACATGAGAAAGCACTGAGAGATGAGATTAAGGCCCTC 480
Db 494 GAACTGACAGAGATGTTCAAGAGAAATGACAAATTTTGGAGAGCAAAATTAAGAACTC 553
QY 481 ACTATGAGCTGCAAAAACAAGAG 505
Db 554 AATTCCTTCTGCAACCAATTTGG 578

RESULT 3
US-10-424-599-32218 ; Sequence 32218, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 32218
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1
US-10-424-599-32218

Query Match 35.5%; Score 308.2; DB 13; Length 933;
Best Local Similarity 75.6%; Pred. No. 3.1e-77;
Matches 382; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 1 ATGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGGTGACC 60
Db 107 ATGGAGGAGGGTAAAGATTGATCAAAAGATTGAGAACTCAAGCAACGGAAGTTACC 166
QY 61 TATCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGATCACTGTTCTATGTAT 120
Db 167 TATCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGATTAATGTTCTATGTAT 226
QY 121 GCTAAAGTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 180
Db 227 GCTCAAGTTCCCTTATCATCTTGTGTCCTGGAAGATGATGATGATGATGATGAT 286
QY 181 TCACTACGCTGACAGAAATCTTGGACAAATACCATGAGACATCTGGAAGAGAGATTGAG 240
Db 287 TCACTACGCTGACAGAAATCTTGGACAAATACCATGAGACATCTGGAAGAGAGATTGAG 346
QY 241 GATGCTAAGATGAGAACTCTCAGCAATGAAAGTGATGAGTCAAGAAAGCAATGACAC 300
Db 347 GATGCTAAGATGAGAACTCTCAGCAATGAAATGATGATGATGATGATGATGATGATGAT 406

QY 301 ATGCAAGTAGAGCTCAGGACATCTGAAGGAGAGATATCATTCATTGAAACCTATGAG 360
DB 407 ATGCAATTTAGAGCTCAGGACCTTGAAGGAGAGACATCGTCACTGAAATTAAGGAA 466
QY 361 CTGATGGCTTTAAGAGAGACATTTGAAATGCGCTTAAAGTATCCGGGACAAAGCATGCC 420
DB 467 CTGATGGCTCTAGAGAGATGCGCTTGAATAATGCGCTCAGTGAAGTCCGTAGAAAAGATG 526
QY 421 AAGTGGCTGACATGATGAGAGACATGGAAGGACATGGAAGATGAGAAATTAAGCGCTC 480
DB 527 GAAGTGCACAGATGTTCAAGAAATGACAAAGATTTGGAGAGAGCAAAATTAAGAACTC 586
QY 481 ACTTATGAGCTGCAAAAACAAACAG 505
DB 587 AATTTCCTCTGCACACACATTTGG 611

RESULT 4
US-09-732-627A-3282
Sequence 3282, Application US/09732627A
Publication No. US2004012338A1
GENERAL INFORMATION:
APPLICANT: Fincher, Karen L.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51770)B
CURRENT APPLICATION NUMBER: US/09/732,627A
CURRENT FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 4930
SEQ ID NO 3282
LENGTH: 535
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3493-014-P1-M1-C8
US-09-732-627A-3282

Query Match 35.4%; Score 307; DB 12; Length 535;
Best Local Similarity 75.7%; Pred. No. 4.9e-77;
Matches 393; Conservative 0; Mismatches 125; Indels 1; Gaps 1;
QY 10 GGGAGGTTGAGTCAAGAGATGAGAACTCAAGTACAGGACGAGTGAACCTTCACTCAAG 69
DB 1 GGGAGGTTGAGTCAAGAGATGAGAACTCAAGTACAGGACGAGTGAACCTTCACTCAAG 60
QY 70 AGGAGGATGGGATTTATCAAGAGGCAAGGAGATCCTGTTCTATGATGCTAAAGTA 129
DB 61 AGGAGGATGGGATTTATCAAGAGGCAAGGAGATCCTGTTCTATGATGCTAAAGTA 120
QY 130 TCTCTTATCATTTATTTCTAGCTCTGGAGATGAGTGAATCTGACAGCCCTTCACTAG 189
DB 121 TCTCTTATCATTTCTGCTAGTCTGGAGATGAGTGAATCTGACAGCCCTTCACTAG 180
QY 190 CTGACAGAAATCTTGGACAAATACATGAGACATCTGGAGAGAAATGTTGGAGATGCTAG 249
DB 181 TTGATGATATTTTGGACCAATATCA-GAAAACCTTGGAGAAAGTATGGAGATGCTAAA 239
QY 250 CATAGAAACCTCAGCAATGAGTGAATGAGTCAAGTCAAGAAAGCATGACAGATGCAAGTA 309
DB 240 CATAGAAATCTCAGCAATGAGTGAATGAGTCAAGTCAAGAAAGCATGAGTCAAGTAT 299
QY 310 GAGCTCAGCATCTGAAGGAGAGATATCAATCATTTGAACATGTAAGCTGATGAGGCC 369
DB 300 GAGCTCAGCATCTGAAGGAGAGATATCAATCATTTGAACATGTAAGCTGATGAGGCC 359
QY 370 TTAGGAGAGACCTTTGAAATGCGCTTCAAGTATCCGGGACAGAGCTCCAAATTTGCTC 429
DB 360 TTAGGAGAGACCTTTGAAATGCGCTTCAAGTATCCGGGACAGAGCTCCAAATTTGCTC 419
QY 430 GACATGATGAGAGCAATGAGAGAGCACTGGAAGTGAAGTAAAGCGCTTCACTTATGAG 489
DB 420 GATATGCAAGAAATTAAGAAATTTCTTGGAGAGAGCAATTAAGCAACTCAATTTCAAT 479

QY 490 CTGCAAAAACACAGAGATGAAATTAAGAGATGTTG 528
DB 480 GTGAATCAACAGCAACTGATCTTATGAAATGTTGAGAGAG 518

RESULT 5
US-10-021-323-8899
Sequence 8899, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Peng, Paul C. C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 8899
LENGTH: 649
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(649)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-021-Q1-K6-C2
US-10-021-323-8899

Query Match 34.9%; Score 303.2; DB 17; Length 649;
Best Local Similarity 70.4%; Pred. No. 6.7e-76;
Matches 455; Conservative 0; Mismatches 173; Indels 18; Gaps 3;
QY 8 GTGGAGGTTGAGTCAAGAGATGAGAACTCAAGTACAGGACGAGTGAACCTTCACTCA 67
DB 3 GGGAGGATTTAGATCAATGAGATGAGAACTCAAGTACAGGACGAGTGAACCTTCACTCA 62
QY 68 AGGAGGATGGGATTTATCAAGAGGCAAGGAGATCACTGTTTATGATGCTAAAG 127
DB 63 AGGAGGATGGGATTTATCAAGAGGCAAGGAGATCACTGTTTATGATGCTAAAG 122
QY 128 TATCTTATCATTTATTTCTAGCTCTGGAGATGAGTGAATATGACAGCCCTTCACTCA 187
DB 123 TTTCTTATTTATTTCTTGTAGTCTTGGCAAGTACAGAGATGCAAGCCCTTCTACTA 182
QY 188 CCGTCAAGAAATCTTGGACAAATACATGACAAATCTGGAGAGAAATGTTGGAGATGCTA 247
DB 183 ATTGTGATATTTTGGACCAATATCAGAAAGCTTCGGGAGAAAGTATGGAGATGCTA 242
QY 248 AGCATGAGAACTCAGCAATGAGTGAATGAGTGAAGAAACAAATGACAGATGCAAG 307
DB 243 AACATGAGAACTCAGCAATGAGTGAATGAGTGAAGAAACAAATGAGTGAAGTCAAG 302
QY 308 TAGAGCTCAGCATCTGAAGGAGAGATATCAATCATTTGAACATGTAAGCTGATGAG 367
DB 303 TTGAATGAGCATTTGAAAGGAGAGATATCACTCTTGTGCTTAAAGAGAGCTGATGAG 362
QY 368 CTTAAGAGAGACCTTGAATAATGCGCTTCAAGATCCGGGACAGAGCTCCAGTTGAG 427
DB 363 CATATAGAGATGCGCTTGAATAATGCGCTTCAAGATCCGGGACAGAGCTCCAGTTGAG 422
QY 428 TCGACATGATGAGAGCAATGAGAAAGGACCTGGAAGTGAAGTGAAGTGAAGTGAAGTGA 487
DB 423 TTGATTAAGCAAGAAATTAAGAAATTTCTTGAAGAGAGCAATTAAGAGAGCTCAAGTTCA 482
QY 488 AGCTGCAAAAACACAGAGATGAAATTAAGAGATGAGAAATGAGAAATGAGTGAAGTGA 547
DB 483 TTCTGATCAACACAA-AGTGCCTTATGAAAGTGAAGAGAG-CAGATGATCATGAT 539

QY 541 AATGGTATCATGAGGAGGAGCTGGGAACTACAGAACACGAGAGATACCTTT 600
 Db 710 AATGGGTTGATCAAG-----CGTAAGAGATTACATTCATCCATATGCCATTT 757
 QY 601 GCGTTCGCGCTGAGGCTTATTCAGCCAAATCTCCAGAGAGATCTAAT 649
 Db 758 GCGTTCGCGTGAAGGCTATGAGCCAAATCTTCAGAAAGATCTAAT 806

RESULT 8

US-09-732-627A-4667
 ; Sequence 4667, Application US/09732627A
 ; Publication No. US2004012338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fincher, Karen L.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(51770)B
 ; CURRENT APPLICATION NUMBER: US/09/732.627A
 ; PRIORITY FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 4930
 ; SEQ ID NO 4667
 ; LENGTH: 474
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3493-037-PI-M1-A1
 US-09-732-627A-4667

Query Match 34.7%; Score 301.2; DB 12; Length 474;
 Best Local Similarity 80.9%; Pred. No. 2,1e-75;
 Matches 351; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 AATGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTCAAGGAGGAGTACC 60
 Db 41 AATGGGAGAGGCAAGATTGAGATCAAGAGATTGAGAACTCAAGTCAAGGAGGAGTACC 100
 QY 61 TATCCCAAGAGAGGAGGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGAT 120
 Db 101 TATCCCAAGAGAGGAGGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGAT 160
 QY 121 GCTAAGATCTCTTATCATTTATTTCTAGCTCTGGGAAAGTGGTGAATCTGAGCCCT 180
 Db 161 GCTAAGATCTCTTATCATTTATTTCTAGCTCTGGGAAAGTGGTGAATCTGAGCCCT 220
 QY 181 TCAACTAGCTGACAGAAATTTTGACAAATACATGAGCAATCTGGGAAAGTGGTGG 240
 Db 221 TCTACTAGTGTGATGATTAATTTGACCAATATCAAGAACTCTGGGAAAGTGGTGG 280
 QY 241 GATCTAAGCATGAGAACTCTGAGCAATGAAGTGAATGAGTCAAGAAAGCAATGACAGC 300
 Db 281 GATCTAAGCATGAGAACTCTGAGCAATGAAGTGAATGAGTCAAGAAAGCAATGATGAGC 340
 QY 301 ATGCAAGTAGAGCTCAGGCACTGAGAGGAGAGATTCACATATTGAAACCATGTAGAG 360
 Db 341 ATGCAAGTAGAGCTCAGGCACTGAGAGGAGAGATTCACATATTGAAACCATGTAGAG 400
 QY 361 CTGATGGGCTTAGAGGAAAGCACTGAAATGAGCTTCAAGTATCCGAGCAAGCACTCC 420
 Db 401 CTGATGGGCTTAGAGGAGAGCCCTCGAAATGAGCCCTTACCTGTGCGTCAAGCAAGT 460
 QY 421 AAGTTCGTGACAT 434
 Db 461 GATGTTCTGATAT 474

RESULT 9

US-10-021-323-13542
 ; Sequence 13542, Application US/10021323
 ; Publication No. US20040123340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deikman, Jill

APPLICANT: Feng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(52274)B
 ; CURRENT APPLICATION NUMBER: US/10/021.323
 ; PRIORITY FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: US 60/255, 619
 ; NUMBER OF SEQ ID NOS: 17880
 ; SEQ ID NO 13542
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(601)
 ; OTHER INFORMATION: unsure at all n locations
 ; OTHER INFORMATION: Clone ID: LIB3829-012-Q6-K6-A7
 US-10-021-323-13542

Query Match 34.2%; Score 296.6; DB 17; Length 601;
 Best Local Similarity 74.4%; Pred. No. 5e-74;
 Matches 374; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 3 GGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTCAAGGAGGAGTACCCTA 62
 Db 33 GGGAGGAGGAGAGATTGAGATCAAGAGATTGAGAACTCAAGTCAAGGAGGAGTACCCTA 92
 QY 63 CTCGAAGAGAGAGGAGGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGATGC 122
 Db 93 TTCGAAGAGAGAGGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGATGC 152
 QY 123 TAAATATCTCTTATCATTTATTTCTAGCTCTGGGAAAGTGGTGAATCTGAGCCCTTC 182
 Db 153 TAAATATCTCTTATCATTTATTTCTAGCTCTGGGAAAGTGGTGAATCTGAGCCCTTC 212
 QY 183 AACTAGCTGACAGAAATCTTGACAAATACCATGAGCAATCTGGGAAAGTGGTGG 242
 Db 213 TACTAATTTGTCGATATTTTGGACCAATATCAGAAAGCTCCGGAAGAGTTATGGGA 272
 QY 243 TGTATAGCATGGAACCTCAGCAATGAGTGAATGAGTCAAGAAAGCAATGACAT 302
 Db 273 TGTATAGCATGGAACCTCAGCAATGAGTGAATGAGTCAAGAAAGCAATGACAT 332
 QY 303 GCAAGTAGAGCTCAGGCACTGAGAGGAGAGATTCACATATTGAAACCATGTAGAGCT 362
 Db 333 GCAAGTAGAGCTCAGGCACTGAGAGGAGAGATTCACATATTGAAACCATGTAGAGCT 392
 QY 363 GATGGCTTAGAGGAGCACTTGAATATGCTTTCAGAGTATCCGAGACAGCATCCAA 422
 Db 393 GATGGCTTAGAGGAGCACTTGAATATGCTTTCAGAGTATCCGAGACAGCATCCAA 452
 QY 423 GTTCGTCGACATGAGAGAGCAATGAGAAAGGAGCACTGGAAGTGAATTAAGCGCTCAC 482
 Db 453 GTTCGTCGACATGAGAGAGCAATGAGAAAGGAGCACTGGAAGTGAATTAAGCGCTCAC 512
 QY 483 TTATGAGCTGCAAAAACAACAG 505
 Db 513 TTTCATTTGAAATCAACAACAG 535

RESULT 10

US-10-021-323-8682
 ; Sequence 8682, Application US/10021323
 ; Publication No. US20040123340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Feng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants
 FILE REFERENCE: 38-21(52274)B
 CURRENT APPLICATION NUMBER: US/10/021,323
 CURRENT FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: US 60/255, 619
 PRIOR FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 17880
 SEQ ID NO 8682
 LENGTH: 639
 TYPE: DNA
 ORGANISM: *Gossypium hirsutum*
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(639)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: LIB828-014-Q1-K6-G9
 US-10-021-323-8682

Query Match 34.2%; Score 296.6; DB 17; Length 639;
 Best Local Similarity 74.4%; Pred. No. 5.2e-74;
 Matches 374; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

Qy	3	GGGACGTGGGAAGCTTGAATCAAGAGATTGGAATCAAGTAAACAGGCAAGTGAACCTA	62
Db	25	GGGAGAGGGGAGATTTGAGTCAAGAGATTGGAATCAAGTAAACAGGCAAGTGAACCTA	84
Qy	63	CTCAAGAGAGAGATGGATTATCAAGAGAGCAAGAGATCACTGTTCTATGTATGC	122
Db	85	TTCAAGAGAGAGATGGATTATCAAGAGAGCAAGAGATCACTATCTGTGTATGC	144
Qy	123	TAAAGTATCTCTTATCATTTATCTAGCTCTGGGAAGATGTTGAATCTGCAAGCCCTTC	182
Db	145	TAAAGTTCTCTTATCATTTATCTAGCTCTGGGAAGATGTTGAATCTGCAAGCCCTTC	204
Qy	183	AATACGTGACAGAAATCTTGACCAATATCAATGACATCTGGGAAGATGTTGGA	242
Db	205	TACTAATTTGGTGAATTTTGGACCAATATCAAGAGATCTCCGGGAAGATTTGGA	264
Qy	243	TGCTAAGCATGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGATGAT	302
Db	265	TGCTAAGCATGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGATGAT	324
Qy	303	GCAAGTAGAGCTCAGGATCTGGAAGGAGAGATGATGATGATGATGATGATGATGATGAT	362
Db	325	GCAAGTAGAGCTCAGGATCTGGAAGGAGAGATGATGATGATGATGATGATGATGATGAT	384
Qy	363	GATGCTCTTGAAGAGCACTTGAAGATGCTTCAAGTATCCGGACCAAGCATGCCA	422
Db	385	GATGCTCTTGAAGAGCACTTGAAGATGCTTCAAGTATCCGGACCAAGCATGCCA	444
Qy	423	GTTGCTGAGCATGATGAGAGCAATGAGCAAGGCACTGGAAGATGATGATGATGATGATGAT	482
Db	445	TGTCCTTGAAGAGCAATGAGCAAGGCACTGGAAGATGATGATGATGATGATGATGATGAT	504
Qy	483	TTATGAGCTGCAAAAACCAACAG 505	
Db	505	TTTCAATCTGAATCAACACAG 527	

RESULT 11
 US-10-278-536-238
 Sequence 238, Application US/10278536
 Publication No. US2003013186A1
 GENERAL INFORMATION:
 APPLICANT: Samaha, Raymond
 APPLICANT: Heard, Jacqueline
 APPLICANT: Uiang, Cal-Zhong
 APPLICANT: Pineda, Omaira
 APPLICANT: Reuber, Lynne
 APPLICANT: Riechmann, Jose-Luis
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Keddie, James
 APPLICANT: Ratcliffe, Oliver

APPLICANT: Piglitim, Marsha
 APPLICANT: Adam, Luc
 APPLICANT: Broun, Pierre
 TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
 FILE REFERENCE: NBI-011
 CURRENT APPLICATION NUMBER: US/10/278,536
 CURRENT FILING DATE: 2002-10-22
 PRIOR APPLICATION NUMBER: 60/125,814
 PRIOR FILING DATE: 1999-03-23
 NUMBER OF SEQ ID NOS: 238
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 238
 LENGTH: 896
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 OTHER INFORMATION: G134
 US-10-278-536-238

Query Match 30.6%; Score 265.2; DB 15; Length 896;
 Best Local Similarity 68.0%; Pred. No. 6.1e-65;
 Matches 385; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

Qy	1	ATGGACGTGGGAAGCTTGAATCAAGAGATTGGAATCAAGTAAACAGGCAAGTGAACCTA	60
Db	24	ATGGGTGAGGAAAGATCGATTAAGAGGATGAGAACCAACAGAGTGTGACG 83	
Qy	61	TACTCCAGAGAGAGATGGATTATCAAGAGAGCAAGAGATCACTGTTCTATGTAT	120
Db	84	TTCTCAAGAGAGAGATGGATTATCAAGAGAGCAAGAGATCACTGTTCTATGTAT	143
Qy	121	GCTAAGTATCTTATCATTTATTTAGCTCTGGAAGATGTTGAATCTGCAAGCCCT	180
Db	144	GCAAAAGTTCCCTCATTAATCTTTGCAAGTAAATGTTAATGATTAATCACTGTTCTCT	203
Qy	181	TCAACTAGCTGACAGAAATCTTGCAAAATATCAAGCAATCTGGAAGAGAGTGTG	240
Db	204	TCATGATTTTGGTCTATGTTGACCAATACCAAGTATCTTGGCAAGAACTATG	263
Qy	241	GATGCTAAGCATGAGAACTCAGCAATGAAGTGAATGATGATGATGATGATGATGATGAT	300
Db	264	GATGCTAAGCATGAGAACTCAGCAATGAAGTGAATGATGATGATGATGATGATGATGAT	323
Qy	301	ATGCAATGAGCTCAGGATCTGGAAGGAGAGATATCATCATTTGAACCATGTAG	360
Db	324	TTACMACTGAGCTCAGGATCTGGAAGGAGAGATATCATCATTTGAACCATGTAG	383
Qy	361	CTATGCTCTTGAAGAGCACTTGAAGATGCTTCAAGTATCCGGACCAAGCATGCC	420
Db	384	CTATGCTCTTGAAGAGCACTTGAAGATGCTTCAAGTATCCGGACCAAGCATGCC	443
Qy	421	AAGTGTGCAATGATGAGAGCAATGGAAGGCACTGGAAGATGATGATGATGATGATGAT	480
Db	444	GAGATCTCTTATCAAGAGAGCAATGGAAGATGATGATGATGATGATGATGATGATGAT	503
Qy	481	ACTTATGAGCTGCAAAAACCAAGAGATGAATAAAGATGATGATGATGATGATGATGAT	540
Db	504	ACTTTCAGCTGC--AAACAAGAGATGCTTATGCAAGCAACCAAGAGATGATG	560
Qy	541	AATGGTATCATCAGAGCAAGCTGG 566	
Db	561	ATGAGAGATCATGATGCGCAGTTTG 586	

RESULT 12
 US-10-412-699B-55
 Sequence 55, Application US/10412699B
 Publication No. US20040045049A1
 GENERAL INFORMATION:
 APPLICANT: Mendel Biotechnology, Inc.
 APPLICANT: Zhang, James
 APPLICANT: Fromm, Michael E.
 APPLICANT: Heard, Jacqueline E.

APPLICANT: Riechmann, Jose Luis
 APPLICANT: Adam, Luc J.
 APPLICANT: Broun, Pierre E.
 APPLICANT: Pineda, Omalra
 APPLICANT: Reuber, T. Lynne
 APPLICANT: Keddle, James S.
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Jiang, Cai-Zhong
 APPLICANT: Samana, Raymond R.
 APPLICANT: Pilgrim, Marsha L.
 APPLICANT: Creelman, Robert A.
 APPLICANT: Dubell, Arnold N.
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Kumimoto, Roderick
 APPLICANT: Sherman, Bradley K.
 TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
 FILE REFERENCE: WBI-0048CIP
 CURRENT APPLICATION NUMBER: US/10/412,699B
 PRIOR FILING DATE: 2003-04-10
 PRIOR APPLICATION NUMBER: 09/394,519
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: 09/489,376
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: 09/506,720
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: 09/533,030
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,392
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,029
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/532,591
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,648
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/713,994
 PRIOR FILING DATE: 2000-11-16
 PRIOR APPLICATION NUMBER: 09/819,142
 PRIOR FILING DATE: 2001-03-27
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 2011
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 55
 LENGTH: 914
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 OTHER INFORMATION: G134
 US-10-412-699B-55

Query Match 30.6%; Score 265.2; DB 13; Length 914;
 Best Local Similarity 68.0%; Pred. No. 6,1e-65;
 Matches 385; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

QY 1 ATGGAGCGTGGAGGTTGAGATCAAGAGATTGAGAACTCACTTAACAGGAGGTGACC 60
 DB 36 ATGGGTAGAGAAAGATGAGATTAAGAGATAGAGAAAGAGAAAGAGAGTGTACG 95
 QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
 DB 96 TTCTCAAGAGAGAGATGGATTGTGTAAGAGGCTAAAGAGATCACAGTTCCTTGTGAT 155
 QY 121 GCTAAAGATCTCTTATGATTTATCTAGCTCTGGGAAAGTGTGATATCTGAGCCCT 180
 DB 156 GCAAAAGTGGCCCTCATATCTTTGCAAGTAAAGTGAAGATGATGATTTACTGTTGCTT 215
 QY 181 TCAACTAGCTGACAGAAATCTTGGACAATACCATGACATCTGGAGAGAGTTGTG 240
 DB 216 TCCATGAGATCTTGGGTATGTTGACCAATACCGAAGTTATCTGGGCAAGAACTATGG 275
 QY 241 GATGCTAAGCATGAGAACTCTGAGCAATGAGTGAAGTCAAGCAAGAAAGATGACAGC 300
 DB 276 GATGCTAAGCATGAGAACTCTGAGCAATGAGTGAAGTCAAGCAAGAAAGATGATGAC 335

QY 301 ATGCAAGTAGAGCTCAGGCATCTGAGAGAGAGATATCAATCATTTGAACCATGTAGAG 360
 DB 336 TTACACTGAGAGCTCAGGCATTTTAAAGGAGAAATATATAGCTCTCTCAACTTGAATAAT 395
 QY 361 CTGATGCGCTTAAAGAGAGCACTTGAATAATGCGCTTACAGTATCCGGGCAAGACAGTCC 420
 DB 396 CTGATGCGCTTAAAGAGAGCACTTGAATAATGCGCTTACAGTATCCGGGCAAGACAGTCC 455
 QY 421 AAGTTCGTCAGATGATGAGAGATGAGAAAGCACTGGAAGATGAGATTAAGCGCTC 480
 DB 456 GAGATCTTATATCAAGAGAGAGAAATGAGAAATGATGCGGAGAGAGCAAGCACTC 515
 QY 481 ACTTATGAGCTGCAAAAACAGAGATGAAATTAAGAGAAATGAGAAATGAGAAATGAGAA 540
 DB 516 ACTTCCAGCTGC--AACCAAGAGATGCGCTATAGCAAGCAAGCAAGAGAGATGAG 572
 QY 541 AATGCTATCATGAG 566
 DB 573 ATGAGAGATCATGAG 598

RESULT 13
 US-10-425-114-26809
 Sequence 26809, Application US/10425114
 Publication No. US2004003488A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(533)3B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 26809
 LENGTH: 1148
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB4606-002-H7_FLI
 US-10-425-114-26809

Query Match 26.9%; Score 233.6; DB 13; Length 1148;
 Best Local Similarity 62.7%; Pred. No. 7.7e-56;
 Matches 400; Conservative 0; Mismatches 229; Indels 9; Gaps 2;

QY 1 ATGGAGCGTGGAGGTTGAGATCAAGAGATTGAGAACTCACTTAACAGGAGGTGACC 60
 DB 287 ATGGGCGCGGAGAGATGAGATTAAGAGATGAGAACTCACTTAACAGGAGGTGACC 346
 QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
 DB 347 TTCTCAAGAGAGAGATGGATTGTGTAAGAGGCTAAAGAGATCACAGTTCCTTGTGAT 155
 QY 121 GCTAAAGTATCTTATGATTTATCTAGCTCTGGGAAAGTGTGATATCTGAGCCCT 180
 DB 407 GCGAGAGTGGCGCTCTCATCTTCTCAAGCGGCGCAAGCTCTACAGCTACTGCTGCGCC 466
 QY 181 TCAACTAGCTGACAGAAATCTTGGACAATACCATGACAACTTGGAGAGAGTTGTG 240
 DB 467 AGGACCTCGCTGTCAGAGATCTTGGAGAGTACCAACCACTCCGGGAAAGTTCTGTG 526
 QY 241 GATGCTAAGCATGAGAACTCTGAGCAATGAGTGAAGTCAAGCAAGAAAGATGACAGC 300
 DB 527 GGTGAAGAGCAAGAACTCTGAGTGAAGTGAAGTCAAGCAAGAAAGATGACAGC 586
 QY 301 ATGCAAGTAGAGCTCAGGCATCTGAGAGAGAGATATCAATCATTTGAACCATGTAGAG 360

Db 587 ATGAGATTACGCTCAGGATCTGAAAGCGAGGAGCTGAACTTCCTCGACCCAGGAG 646
Qy 361 CTGATGCGCTTAAAGAGAGCACTTGAATAATGCTTCAAGTATCCGGGACAAGCATGCC 420
Db 647 CTGATGCGCTTAAAGAGAGGCTTCAAGATGGGAGACCAATGGCGAGAAAGAGATG 706
Qy 421 AAGTTGCTCGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATTAAGCCCTC 480
Db 707 GACTACTGAGAGATGCAAGAGCAATGGAAGATGCTGAGAGCAACCAAGATATCTG 766
Qy 481 ACTTATGAGCTGCAAAAAACAAGAGATGAAAAATAAAGAGATGAGAAACATGAA 540
Db 767 ACTTTAGATGTC---ACCAACAGGCTGTGATCTGAGCGCGGCATGAGGAGCTGGAG 823
Qy 541 AATGGGATATCATGAGAGGAGCTGGGGAATCAACAACAACAGAGAGATACCTTTT 600
Db 824 ACCGATACCATCATGAGTCCAGC-----ACGACAGGATTTCAITTCAGATGCCGCTT 877
Qy 601 GCCTTCGCGTGCAGCCTTATTCAGCCCAATCTCCAGGA 638
Db 878 ACCTTCGCGGTGACGCCACCAACCCCACTTCAGAGA 915

RESULT 14

US-10-437-963-9922
; Sequence 9922, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 9922
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16293C.1
US-10-437-963-9922

Query Match 25.1%; Score 217.8; DB 17; Length 3265;
Best Local Similarity 61.3%; Pred. No. 4,8e-51;
Matches 392; Conservative 0; Mismatches 232; Indels 15; Gaps 2;

Qy 1 ATGGGACGTGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGCGTGACC 60
Db 120 ATGGGCGCGGCAAGTCAAGATCAAGAGATCGAAGATTCAGCAACCGGAGGTGACG 179
Qy 61 TACTCCAGAGAGAGAAATGGAATTAACAAGAGCAAGAGATCACTGTTCTATGTGAT 120
Db 180 TTCTCGAAGCGCGCTCCGGGATCTCAAGAGAGCCCGGAGATGGGCTGCTCGCAC 239
Qy 121 GCTAAGTATCTCTTATCTTATCTTCTGAGTCTGGGAGATGTTGATATCTGACGCCCT 180
Db 240 CCGGAGGTGGGGTGTCTATCTTCTCGACGCGCGCAAGCTCTCGACTTATGACGCC 299
Qy 181 TCACTACGCTGACAGAAATCTTGGACAAATACATGACATCTGGAGAAAGTTGGG 240
Db 300 AAGACCAAGCTGTCAAGATCTTGGAGAAATACCAAGACCACTCCGGGAAATATCTGG 359
Qy 241 GATGCTAAGCATGAGAACTTACGCAATGAATGATGAAGTCAAGAAAGCAATGACAC 300
Db 360 GATGAGAAAGCAAGAGCTCAGCGCAAGATCATGCTGTCTCAAGAAAGAGCAAGAC 419

Qy 301 ATGCAAGTAGAGCTCAGGATCTGAGAGGAGAGATTCATCATGATTGAACATGTAGAG 360
Db 420 ATGCAAGATCGAGCTCAGGATCTGAGAGGAGAGATTCATCATGATTGAACATGTAGAG 479
Qy 361 CTGATGCGCTTAAAGAGAGCACTTGAATAATGCTTCAAGTATCCGGGACAAGCATGCC 420
Db 480 CTGATGCGGATCGAGAGGCGCTTCAACAAACCGCCAGCCCAATCTGCGGGAACAAGATATG 539
Qy 421 AAGTTGCTCGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATTAAGCCCTC 480
Db 540 GACCACTGAGAGATTCATTAAGAAATGAGAGATGCTTGAAGAGACAGCAACAAGATTTG 599
Qy 481 ACTTATGAGCTGCAAAAAACAAGAGATGAAAAATAAAGAGATGAGAAACATGAA 540
Db 600 GCTTTAGAGGTGC---ACGACAGAGGTGAGCTGAGCGCGCATTAAGAGAGCTGGAG 656
Qy 541 AATGGGATATCATGAGAGGAGCTGGGGAATCAACAACAACAGAGAGATACCTTTT 600
Db 657 CTGCGCTACACCA-----CGACGACAGGAGATTTGGCGGCTCGATGCGCTTC 704
Qy 601 GCCTTCGCGTGCAGCCTTATTCAGCCCAATCTCCAGGAG 639
Db 705 ACCTTCAGGGGTGACGCCACCAACCCCACTTCAGAGAG 743

RESULT 15

US-10-425-114-4580
; Sequence 4580, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4580
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700382572_FLI
US-10-425-114-4580

Query Match 25.0%; Score 216.8; DB 13; Length 657;
Best Local Similarity 64.6%; Pred. No. 3.5e-51;
Matches 323; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 1 ATGGGACGTGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTACAGGAGCGTGACC 60
Db 136 ATGGGCGCGGCAAGTCAAGATCAAGAGATCGAAGATCTTAACAACCGGAGGTGACC 195
Qy 61 TACTCCAGAGAGAGATGGAATTAACAAGAGCAAGAGATCACTGTTCTATGTGAT 120
Db 196 TTCTCGAAGCGCGGCGGACTGTCAAGAGAGCAAGGAGATGGCTGCTCGCAC 255
Qy 121 GCTAAGTATCTCTTATCTTATCTTCTGAGTCTGGGAGATGTTGATATCTGACGCCCT 180
Db 256 GCCGAGTGGGGTGTCTATCTTCTCGACGCGCGCAAGCTCTAGAGATATGCTCGCCC 315
Qy 181 TCACTACGCTGACAGAAATCTTGGACAAATACATGACATCTGGAGAAAGTTGGG 240
Db 316 AGGACCTGCTGTCAAGATCTTGGAGAAATACCAAGACCACTCCGGGAAATATCTGG 375
Qy 241 GATGCTAAGCATGAGAACTTACGCAATGAATGATGAAGTCAAGAAAGCAATGACAC 300

```

Db      376  GGTGAGAAACACAAGAACTGAGTGCAAGATCGACAGATCAAGAAGAGAACGACAAAC 435
QY      301  ATGCAGTAGAGCTCAGGCACTGGAAGGAGAGATATCATCATTTGAACCATGTAGAG 360
Db      436  ATGCAGATTCAAGCTCAGGCACTGGAAGGAGAGATATCATCATTTGAACCATGTAGAG 495
QY      361  CTGATGACCTTAAAGAGCACTTGAATGACCTTACAAATATCGGAGCAAGCAATCC 420
Db      496  CTGATGACCTTAAAGAGGAGGCTTCAAGATGAGCAAGCAATATCGGAGCAAGCAATG 555
QY      421  AAGTTCGTGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATTAGCCCTC 480
Db      556  GACTACTGAGAGATGCAAGACGAAATGGAAGATGCTGAGAGACGAAACAAAGATATCTG 615
QY      481  ACTTATGAGCTGCATAAACA 500
Db      616  ACTTTAGATGCAACCAACA 635

```

Search completed: September 25, 2004, 22:22:17
 Job time : 478.636 secs

QY	ATGGGACGTGGGAAGCTTAGATCAAGAGGATTTGGAACTCAATTAACAGGACAGTACCC	60
QY	1 ATGGGTGCTGGAAAGATTGAATCAAGAAAGATCGAAAACCCCAAAACAGCAAGTACCC	60
DB		
QY	61 TATCCCAAGAGAGGAAATGAGATTATCAAGAAGCGAAGAGATCACTGTTCTATGTGAT	120
DB	61 TATCCCAAGAGAAATATGTAATTTTCAAGAAAGCCCAAGAACTCACTGTAATTTTGAT	120
QY	121 GCTAAAGATCTTATTCATTTATTTATCTAGCTCTGGAAAGATGGTTGAATACTGCAGCCCT	180
QY	121 GCTAAAGATCTCTTTATTCATGTTCTCCCAACTAACAATCAATGAGTATCATTAAGCCCC	180
DB		
QY	181 TCAACTACGCTGCAGAAAATCTTTGACAATTCATGAGCAATCTGGGAAAGATTGGG	240
DB	181 TCCCATCGCAAAAGAAAGATCTTACGATTCATATTCAGAAAGCTTTAGGATAGATCTGGG	240
QY	241 GATCTTAAGCATGAGAACTCTACGCAATGAATGCGATAGAGTCACAAAGACAATAGACAGC	300
DB	241 GGCACTCAATATGAGAAAATGCAAGAGCACTTGAGAGAGCTGATATGATATCATTAAG	300

QY 301 ATGCAAGTAGAGCTCAGGATCTGTAAGGAGAGATATCATCATTTGAACCATGTAGAG 360
DB 301 CTGACACAGAAATACGACGAGAGAGAGGCGCTGATGATGATGATGATGATGAT 360
QY 361 CTGATGGCTTGAAGAGAGCACTTGAATAATGCGCTTCAAGTATCCGGGACAGCATGCC 420
DB 361 CTGGCGGCTTGTGAGCAACATATGATGAGAGCCCTGAAATGTTGCGTGGCAGAGATGAC 420
QY 421 AAGTTCGTGACA 433
DB 421 CATGTGATCAAAA 433

RESULT 2

US-09-410-464-2
Sequence 2, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
EARLIER FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 946
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-09-410-464-2

Query Match 17.1%; Score 148.2; DB 4; Length 946;
Best Local Similarity 58.9%; Pred. No. 9.9e-33;
Matches 255; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGGAGCTGGGAGAGTTGATGATCAAGAGAGATTGAGAACTCAAGTAAACAGGAGTGACC 60
DB 1 ATGGGCTGTGAGAAAGATTGAAATCAAGAAATCGAAACCTCAACAAAGCGCAAGTCAACC 60
QY 61 TACTCCAGAGAGAGATGGGATTTATCAAGAAAGCAAGAGATGATGATGATGATGAT 120
DB 61 TACTCCAGAGAGAGATGGGATTTATCAAGAAAGCAAGAGATGATGATGATGATGAT 120
QY 121 GCTAAGTATCTTTATCATTTATTTAGCTTGGGAGAGTGGTGAATPACTGACGCCCT 180
DB 121 GCTAAGTATCTTTATCATTTATTTAGCTTGGGAGAGTGGTGAATPACTGACGCCCT 180
QY 181 TCAACTACGCTGACAGAAATCTTGAACAAATACATGAGCAATCTGGGAGAGAGTGGG 240
DB 181 TCCACATGACAAAGAGATCTACATGATTCAGAAACGCTTTAGGCAATGATGATGATG 240
QY 241 GATGCTAAGCATGAGAACTTCAAGCAATGATGATGATGATGATGATGATGATGATG 300
DB 241 GGCACCTCATATGAGAAATATGCAAGAGCACTTGAAGAGTGAATGATATCATATCAAT 300
QY 301 ATGCAAGTAGAGCTCAGGATCTGAAAGGAGAGATATCATCATTTGAACCATGTAGAG 360
DB 301 CTGACACAGAAATACGACGAGAGAGAGAGGCGCTGATGATGATGATGATGATGATGAT 360
QY 361 CTGATGGCTTGAAGAGAGCACTTGAATAATGCGCTTCAAGTATCCGGGACAGCATGCC 420
DB 361 CTGGCGGCTTGTGAGCAACATATGATGAGAGCCCTGAAATGTTGCGTGGCAGAGATGAC 420
QY 421 AAGTTCGTGACA 433
DB 421 CATGTGATCAAAA 433

DB 421 CATGTGATCAAAA 433

RESULT 3

US-09-410-464-1
Sequence 1, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
EARLIER FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4285
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-1

Query Match 12.6%; Score 109; DB 4; Length 4285;
Best Local Similarity 73.5%; Pred. No. 3.9e-21;
Matches 139; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGGAGCTGGGAGAGTTGATGATCAAGAGAGATTGAGAACTCAAGTAAACAGGAGTGACC 60
DB 2001 ATGGGCTGTGAGAAAGATTGAAATCAAGAAATCGAAACCTCAACAAAGCGCAAGTCAACC 2060
QY 61 TACTCCAGAGAGAGATGGGATTTATCAAGAAAGCAAGAGATGATGATGATGATGATGAT 120
DB 2061 TACTCCAGAGAGAGATGGGATTTATCAAGAAAGCAAGAGATGATGATGATGATGATGAT 120
QY 121 GCTAAGTATCTTTATCATTTATTTAGCTTGGGAGAGTGGTGAATPACTGACGCCCT 180
DB 121 GCTAAGTATCTTTATCATTTATTTAGCTTGGGAGAGTGGTGAATPACTGACGCCCT 180
QY 181 TCAACTACG 189
DB 2181 TCCACATG 2189

RESULT 4

US-08-904-284-1
Sequence 1, Application US/08904284
Patent No. 6133435
GENERAL INFORMATION:
APPLICANT: Fernandez, Donna E.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: EXPRESSION OF AGU1.5 SEQUENCE IN
TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-904-284-1

Query Match 12.2% Score 105.6; DB 3; Length 1070;
Best Local Similarity 55.9%; Pred. No. 1.7e-20;
Matches 229; Conservative 0; Mismatches 169; Indels 12; Gaps 1;

QY 1 ATGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGTGACC 60
DB 19 ATGGCTGTGGAAAATCGAGATAAGAGATCGAAGATCGAATAGCAGACAACTCACT 78
QY 61 TACTCCAAAGGAGGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGAT 120
DB 79 TTTTCCAAAGAGGGGTTCTGGTTACTTAAAGAAAGCTGTGAGCTCTCTGTTCTTGTGAT 138
QY 121 GCTAAAGTATCTCTTATCATTTTATCTAGCTCTGGAGATGGTTGATTAATCTGACGCCCT 180
DB 139 GCTGAAGTCTGTGATCGTCTCTCTCTAAGTCTGGAGAGCTCTTCGAGTACTCACTACT 198
QY 181 TCAACTACGCTGACAGAAATCTTGACAAATACCATGACAACTCTGGAGAAAGTTGTGG 240
DB 199 GGAATGAGCAACACTTTCAGATACGATACCA-----CCAGATTCTTCA 246
QY 241 GATGCTAAGATGAGAACTCAGCAATGAGTGAATGAGTCAAGAAAGCAATGACAGC 300
DB 247 GCTTCTTAAGCAGAGAGGATTTGGCAGAGGTGATTTTAAAGATCAACTTCAAG 306
QY 301 ATGCAAGTAGAGCTCAGGCACTTGAGAGGAGAGATATCAATCATTTGAACATGTAGAG 360
DB 307 CTTCAAGAGAAACTTTTACAACCTGACAGGCGCAAGGCTTGAATCCTGACCTTTAAAGAG 366
QY 361 CTGATGCTTGAAGAGAGCACTTGAAATGGCTTACAGATATCCGGGA 410
DB 367 CTGCAAGCCTTGAGCAGCACTATATCATGATGATTTACTGTCAAGA 416

RESULT 5
US-08-904-284-6
Sequence 6, Application US/08904284
Patent No. 613935
GENERAL INFORMATION:
APPLICANT: Fernandez, Donna E.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: EXPRESSION OF AGLIS SEQUENCE IN
TITLE OF INVENTION: TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2437 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-904-284-6

Query Match 10.8% Score 93.6; DB 3; Length 2437;
Best Local Similarity 70.0%; Pred. No. 7.5e-17;
Matches 126; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 ATGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGTGACC 60
DB 527 ATGGCTGTGGAAAATCGAGATAAGAGATCGAAGATCGAATAGCAGACAACTCACT 586
QY 61 TACTCCAAAGGAGGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGAT 120
DB 587 TTTTCCAAAGAGCGCTTGGGTTACTTAAAGAAAGCTGTGAGCTCTCTGTTCTTGTGAT 646
QY 121 GCTAAAGTATCTCTTATCATTTTATCTAGCTCTGGAGATGGTTGATTAATCTGAGGCCCT 180
DB 647 GCTGAAGTCTGTGATCGTCTCTCTCTAAGTCTGGCAAGCTCTTGAATCTCAAGTACT 706

RESULT 6
US-08-867-087B-12
Sequence 12, Application US/08867087B
Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
STREET: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-867-087B-12

Query Match 10.8%; Score 93.4; DB 2; Length 1043;
Best Local Similarity 53.8%; Pred. No. 5.4e-17;
Matches 218; Conservative 0; Mismatches 181; Indels 6; Gaps 1;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGACTCAAGTAAACAGGAGGTGACC 60
DB 34 ATGGGGAGGGGAGAGATTGAGCTGAGAGCGCATGAGAAACAATCAACAGGACAGTCAAC 93
QY 61 TACTCCAGAGGAGGAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
DB 94 TTCTCCAGAGGCGGCAACGCGCTCTCAAGAGGCTTACAGAGCTGTCCCTCTCTGCGAC 153
QY 121 GCTAAGTATCTCTTATCACTTATTTAGCTCTGGAGAGTGTGAATATGACAGCCCT 180
DB 154 GCGGAGTCCGCGCTCATCTCTTCCAGCCGCGGCAAGCTTACAGAGTCCGCGAGCC 213
QY 181 TCACTACGCTGACAGAAATCTTGAACAATACATGACCAATCTGGGAGAGTGTGG 240
DB 214 GGCATACCAAGACCTTGAAGGTACCAACATGTGTCTACAAAGCTCAAGATTCAC 273
QY 241 GATGTAAGATGAGAACCTCAG-----CAATGAAGTGAATAGAGTCAAGAAACAT 294
DB 274 AATGCACTTTCTGAAACTCAGAGTGTGTACATGAATGTCAAGTTGAAGCAAAATTT 333
QY 295 GACAGATGCAAGTAGAGTCAAGCATCTGAAAGGAGAGATATCAATCATTTGAACCAT 354
DB 334 GAAGCTTTCAGCGCACTCAAGGCACTTGTGGGAGAGATCTTGAACCACTGACGCGTC 393
QY 355 GTAGAGCTATGCGCTTATAGAGAGACCTTGAAGAGGCTTACA 399
DB 394 AAGGAATTGAGAGCTGAGAAACGTTGAATGTGACTATCA 438

RESULT 7

US-08-485-981-9
Sequence 9, Application US/06485981
Patent No. 5861542
GENERAL INFORMATION:
APPLICANT: At. Gynheung
TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarguist Sparkman Campbell Leigh &
ADDRESSEE: Whinston
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,981
FILING DATE: June 7, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449

FILING DATE: October 14, 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-42933
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-485-981-9

Query Match 10.6%; Score 92.2; DB 2; Length 945;
Best Local Similarity 67.4%; Pred. No. 1.1e-16;
Matches 130; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
DB 16 ATGGGAGGGGTAGGTTGAGCTTACAGAAATAGAGAACAGATCAACAGGCAAGTAC 75
QY 61 TACTCCAGAGGAGGAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
DB 76 TTCCCTAAGAGAAATGACCTTTGAAAAAGCTTATGAGCTTCTGTTCTTGTGAT 135
QY 121 GCTAAGTATCTCTTATCACTTATTTAGCTCTGGGAGAGTGTGAATATGACAGCCCT 180
DB 136 GCTAGGTTGCTTCATCATCTTCTCCATATGAGGAGAAACTGACAGTTCGACATGAC 195
QY 181 TCACTACGCTGA 193
DB 196 TCTAGATGCTCA 208

RESULT 8

US-08-867-087B-10
Sequence 10, Application US/08867087B
Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: At. Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarguist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.